

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:26:08 ; Search time 39 Seconds  
(without alignments)  
2507.965 Million cell updates/sec

Title: US-10-036-150-45  
Perfect score: 1617  
Sequence: 1 MRLSGTPTATCCVAIEVLGI.....LISSAFERKPGDIRHPKHVQ 310

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

- Database : SPTREMBL 25:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriaph:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1617	100.0	975	4 Q8NCC9	Q8ncc9 homo sapien
2	1156	71.5	299	4 Q8N866	Q8n866 homo sapien
3	1156	71.5	894	4 Q8NCI4	Q8nci4 homo sapien
4	678	41.9	1734	5 Q86IT5	Q86it5 dictyosteli
5	595	36.8	860	3 Q96X26	Q96x26 yarrowia li
6	590	36.5	897	10 Q9SJY2	Q9sjy2 arabidopsis
7	583	36.1	892	3 Q8TGB2	Q8tgb2 candida alb
8	524	32.4	795	5 Q19870	Q19870 caenorhabdi
9	511.5	31.6	927	5 Q9V4N0	Q9v4n0 drosophila
10	511	31.6	333	6 Q9GM09	Q9gm09 macaca fasc
11	471	29.1	692	10 Q8LNL1	Q8lnl1 oryza sativ
12	421.5	26.1	1077	5 Q7YU86	Q7yu86 drosophila
13	418.5	25.9	1077	5 Q9V8H8	Q9v8h8 drosophila
14	415.5	25.7	884	10 Q9FFI6	Q9ffi6 arabidopsis
15	414	25.6	918	3 O13663	O13663 schizosacch
16	387	23.9	1017	3 Q07830	Q07830 saccharomyc

90	96	5.9	561	10	Q9SB39	Q9sb39 arabidopsis	163	88	5.4	660	16	Q8Z795	Q8z795 salmonella
91	96	5.9	1840	3	Q9HED6	Q9hed6 neurospora	164	88	5.4	660	16	Q83T27	Q83t27 salmonella
92	96	5.9	2109	12	Q8B0H5	Q8b0h5 vesicular s	165	87.5	5.4	385	2	P94599	P94599 bacillus th
93	96	5.9	2163	5	Q9NFB6	Q9nfb6 plasmodium	166	87.5	5.4	413	16	Q81Y95	Q81y95 bacillus an
94	95.5	5.9	532	2	Q9FDB4	Q9fdb4 streptomyc	167	87.5	5.4	465	4	Q8NBN4	Q8nb4 homo sapien
95	95.5	5.9	566	16	Q8D7J1	Q8d7j1 vibrio vuln	168	87.5	5.4	848	2	Q9RAT4	Q9rat4 lactococcus
96	95	5.9	311	5	Q9BLZ3	Q9blz3 renilla mue	169	87.5	5.4	1253	5	Q8WQ61	Q8wq61 drosophila
97	95	5.9	411	2	Q7WUC4	Q7wuc4 escherichia	170	87	5.4	220	10	Q9FP70	Q9fp70 oryza sativ
98	93.5	5.8	542	17	Q8PRQ7	Q8prq7 methanosarc	171	87	5.4	233	10	Q84L55	Q84l55 oryza sativ
99	93.5	5.8	596	16	Q8EF27	Q8ef27 shewanella	172	87	5.4	304	5	Q7YY57	Q7yy57 cryptospori
100	93.5	5.8	1480	10	Q7XLJ7	Q7xlj7 oryza sativ	173	87	5.4	395	13	Q9I9T6	Q9i9t6 lagopus mut
101	92.5	5.7	236	16	Q82MN7	Q82mn7 streptomyc	174	87	5.4	423	17	Q97C46	Q97c46 thermoplasm
102	92.5	5.7	542	17	Q8PRQ2	Q8prq2 methanosarc	175	87	5.4	459	4	Q96SJ4	Q96sj4 homo sapien
103	92	5.7	318	13	Q90XA9	Q90xa9 xenopus lae	176	87	5.4	488	5	Q9N9Z2	Q9n9z2 drosophila
104	92	5.7	320	13	Q13026	Q13026 xenopus lae	177	87	5.4	599	16	Q92RD6	Q92rd6 rhizobium m
105	92	5.7	461	16	Q98QL5	Q98ql5 mycoplasma	178	87	5.4	634	6	Q46600	Q46600 bos taurus
106	91.5	5.7	314	5	Q86D20	Q86d20 caenorhabdi	179	87	5.4	833	5	Q8IFI0	Q8ifi0 trypanosoma
107	91.5	5.7	477	4	Q86YC5	Q86yc5 homo sapien	180	87	5.4	2182	5	Q8II25	Q8iiz5 plasmodium
108	91.5	5.7	503	16	Q7UG72	Q7ug72 rhodopirell	181	86.5	5.3	323	16	Q8F921	Q8f921 leptospira
109	91.5	5.7	542	17	Q8TRV9	Q8trv9 methanosarc	182	86.5	5.3	335	16	Q8PG38	Q8pge8 xanthomonas
110	91.5	5.7	542	17	Q8TQB9	Q8tqb9 methanosarc	183	86.5	5.3	390	5	Q9VA28	Q9va28 drosophila
111	91.5	5.7	542	17	Q8TH47	Q8th47 methanosarc	184	86.5	5.3	424	5	Q8IHE4	Q8ihe4 drosophila
112	91.5	5.7	653	16	Q9PMW6	Q9pmw6 campylobact	185	86.5	5.3	478	16	Q9LI09	Q9li09 streptomyc
113	91.5	5.7	1232	5	Q8VMD2	Q8vmd2 drosophila	186	86.5	5.3	500	16	Q9RXK6	Q9rxk6 streptomyc
114	91.5	5.7	1253	5	Q9W111	Q9w111 drosophila	187	86.5	5.3	527	16	Q8X7U5	Q8x7u5 escherichia
115	91	5.6	421	17	Q9HIJ0	Q9hij0 thermoplasm	188	86.5	5.3	527	16	Q8FJL9	Q8fjl9 escherichia
116	90.5	5.6	217	2	Q8GNK7	Q8gnk7 mycobacteri	189	86.5	5.3	528	16	Q9CP39	Q9cp39 pasteurella
117	90.5	5.6	237	16	Q99VR3	Q99vr3 staphylococ	190	86.5	5.3	1005	5	Q9GR06	Q9gr06 plasmodium
118	90.5	5.6	310	2	Q87616	Q87616 pseudomonas	191	86.5	5.3	1005	5	Q8IIE5	Q8iee5 plasmodium
119	90.5	5.6	327	16	Q92US7	Q92us7 rhizobium m	192	86	5.3	291	16	Q8ZKU2	Q8zku2 salmonella
120	90.5	5.6	422	16	Q8Y778	Q8y778 listeria mo	193	86	5.3	338	12	Q9ITI6	Q9iti6 tupaia herp
121	90.5	5.6	446	10	Q7X605	Q7x605 oryza sativ	194	86	5.3	390	13	Q9I9U3	Q9i9u3 lagopus lag
122	90.5	5.6	485	11	Q9D5R5	Q9d5r5 mus musculu	195	86	5.3	496	1	Q34184	Q34184 halobacteri
123	90.5	5.6	2109	12	Q8B0H0	Q8b0h0 vesicular s	196	86	5.3	532	2	Q9F7M5	Q9f7m5 gamma-prote
124	90.5	5.6	4876	5	Q8MUM9	Q8mum9 drosophila	197	85.5	5.3	419	10	Q9FQ10	Q9fq10 medicago tr
125	90.5	5.6	4904	5	Q9VH01	Q9vh01 drosophila	198	85.5	5.3	422	5	Q8I7J0	Q8i7j0 caenorhabdi
126	90	5.6	291	16	Q8Z2S6	Q8z2s6 salmonella	199	85.5	5.3	442	11	Q8VI87	Q8vi87 mus musculu
127	90	5.6	373	2	Q69067	Q69067 pseudomonas	200	85.5	5.3	512	10	Q84QB2	Q84qb2 oryza sativ
128	90	5.6	399	17	Q8PWD2	Q8pwd2 methanosarc	201	85.5	5.3	516	5	Q21982	Q21982 caenorhabdi
129	90	5.6	596	11	Q8JZW9	Q8jzw9 mus musculu	202	85.5	5.3	685	16	Q88LT9	Q88lt9 pseudomonas
130	90	5.6	660	16	Q8ZP78	Q8zp78 salmonella	203	85	5.3	247	16	Q8ZRH5	Q8zrh5 salmonella
131	89.5	5.5	258	16	Q83R03	Q83r03 s imidazole	204	85	5.3	378	16	Q9AAZ9	Q9aaz9 caulobacter
132	89.5	5.5	291	16	Q92DU8	Q92du8 listeria in	205	85	5.3	389	16	Q7W3T6	Q7w3t6 bordetella
133	89.5	5.5	291	16	Q8Y935	Q8y935 listeria mo	206	85	5.3	389	16	Q7W055	Q7w055 bordetella
134	89.5	5.5	294	16	Q8VJZ7	Q8vjz7 mycobacteri	207	85	5.3	509	16	Q81X77	Q81x77 bacillus an
135	89.5	5.5	300	16	Q06135	Q06135 mycobacteri	208	85	5.3	509	16	Q81SK7	Q81sk7 bacillus ce
136	89.5	5.5	300	16	Q7VEW2	Q7vew2 mycobacteri	209	85	5.3	511	16	Q92IJ2	Q92ij2 rickettsia
137	89.5	5.5	324	16	Q83Z25	Q83z25 enterococcu	210	85	5.3	607	16	Q8DBM0	Q8dbm0 vibrio vuln
138	89.5	5.5	437	16	Q81Z78	Q81z78 bacillus an	211	85	5.3	906	16	Q9RTN7	Q9rtn7 deinococcus
139	89.5	5.5	499	16	Q8P7K2	Q8p7k2 xanthomonas	212	85	5.3	973	16	Q88M14	Q88m14 pseudomonas
140	89.5	5.5	527	16	Q83S32	Q83s32 shigella fl	213	85	5.3	1012	16	Q7UHH9	Q7uhj9 rhodopirell
141	89.5	5.5	548	2	Q9RMJ0	Q9rmj0 neisseria m	214	85	5.3	1723	4	Q9Y4F4	Q9y4f4 homo sapien
142	89.5	5.5	604	17	Q9YCY3	Q9ycz3 aeropyrum p	215	84.5	5.2	381	16	Q9X1R7	Q9xlr7 thermotoga
143	89.5	5.5	816	2	Q9AHT9	Q9aht9 streptococc	216	84.5	5.2	453	4	Q9Y6X5	Q9y6x5 homo sapien
144	89.5	5.5	1339	3	Q8TFJ6	Q8tfj6 kluyveromyc	217	84.5	5.2	480	17	Q9UYU1	Q9uyul pyrococcus
145	89	5.5	481	10	Q8LMP9	Q8lmp9 oryza sativ	218	84.5	5.2	538	11	Q80XK0	Q80xk0 mus musculu
146	89	5.5	700	16	Q9I338	Q9i338 pseudomonas	219	84.5	5.2	545	16	Q9HVN7	Q9hvn7 pseudomonas
147	89	5.5	891	5	Q18602	Q18602 caenorhabdi	220	84.5	5.2	642	3	Q9UU76	Q9uu76 schizosacch
148	89	5.5	2241	12	Q91HJ2	Q91hj2 avian param	221	84.5	5.2	875	2	Q9RAA4	Q9raa4 rickettsia
149	88.5	5.5	424	16	Q92UV8	Q92uv8 rhizobium m	222	84.5	5.2	944	12	Q9DW96	Q9dw96 rat cytomeg
150	88.5	5.5	437	16	Q81IF1	Q81if1 bacillus ce	223	84.5	5.2	1789	5	Q8T145	Q8tl45 dictyosteli
151	88.5	5.5	470	2	Q9X5S1	Q9x5s1 streptomyc	224	84	5.2	285	13	Q7SZ29	Q7sz29 xenopus lae
152	88.5	5.5	480	10	Q8LJR0	Q8ljr0 zea mays (m	225	84	5.2	374	16	P73953	P73953 synechocyst
153	88.5	5.5	802	16	Q97QM8	Q97qm8 streptococc	226	84	5.2	392	5	Q9W253	Q9w253 drosophila
154	88.5	5.5	828	16	Q8DPQ2	Q8dpq2 streptococc	227	84	5.2	426	16	Q8DB10	Q8db10 vibrio vuln
155	88	5.4	367	2	Q84DG7	Q84dg7 escherichia	228	84	5.2	437	10	Q9ASX8	Q9asx8 arabidopsis
156	88	5.4	416	16	Q89KZ1	Q89kz1 bradyrhizob	229	84	5.2	465	5	Q22129	Q22129 caenorhabdi
157	88	5.4	417	16	Q8FRV2	Q8frv2 corynebacte	230	84	5.2	576	2	Q60113	Q60113 zymomonas m
158	88	5.4	427	16	Q9K9G9	Q9k9g9 bacillus ha	231	84	5.2	585	12	Q07041	Q07041 variola vir
159	88	5.4	486	16	Q8FRY2	Q8fry2 corynebacte	232	84	5.2	592	10	Q9FHN6	Q9fhn6 arabidopsis
160	88	5.4	491	10	Q8LPV6	Q8lpv6 deschampsia	233	84	5.2	599	4	Q9H5P1	Q9h5p1 homo sapien
161	88	5.4	525	17	Q8TIZ2	Q8tiz2 methanosarc	234	84	5.2	605	4	Q96MM7	Q96mm7 homo sapien
162	88	5.4	546	2	Q9KJX5	Q9kjk5 flavobacter	235	84	5.2	787	16	Q8F093	Q8f093 leptospira

236	84	5.2	1056	4	Q9H3R0	Q9h3r0 homo sapien	309	81.5	5.0	542	2	Q68872	Q68872 myxococcus
237	83.5	5.2	133	9	Q8SCV7	Q8scv7 pseudomonas	310	81.5	5.0	548	16	Q53560	Q53560 mycobacteri
238	83.5	5.2	347	10	Q93VR8	Q93vr8 arabidopsis	311	81.5	5.0	548	16	Q7TWB7	Q7twb7 mycobacteri
239	83.5	5.2	349	5	Q44538	Q44538 caenorhabdi	312	81.5	5.0	570	10	Q9LU36	Q9lu36 arabidopsis
240	83.5	5.2	468	16	Q93IW3	Q93iw3 streptomyce	313	81.5	5.0	601	16	Q9I3W1	Q9i3w1 pseudomonas
241	83.5	5.2	482	16	Q99R34	Q99r34 staphylococ	314	81.5	5.0	607	10	Q9LGS5	Q9lgs5 oryza sativ
242	83.5	5.2	482	16	Q8NUM8	Q8num8 staphylococ	315	81.5	5.0	694	10	Q7XW53	Q7xw53 oryza sativ
243	83.5	5.2	519	16	Q83BH2	Q83bh2 coxiella bu	316	81.5	5.0	694	16	Q88VS3	Q88vs3 lactobacill
244	83.5	5.2	595	10	Q8W5L8	Q8w5l8 oryza sativ	317	81.5	5.0	898	10	Q9FVE9	Q9fve9 nicotiana t
245	83.5	5.2	595	10	Q7XH72	Q7xh72 oryza sativ	318	81.5	5.0	902	2	Q84F16	Q84f16 clostridium
246	83.5	5.2	726	16	Q8PKI8	Q8pk18 xanthomonas	319	81.5	5.0	930	2	Q59290	Q59290 clostridium
247	83.5	5.2	796	11	Q9IY06	Q9ly06 mus musculu	320	81.5	5.0	940	16	Q9JTX2	Q9jtx2 neisseria m
248	83.5	5.2	861	16	Q88NQ1	Q88nq1 pseudomonas	321	81.5	5.0	965	2	Q9ZHV5	Q9zhv5 neisseria m
249	83.5	5.2	1398	1	Q9P9L1	Q9p9l1 pyrococcus	322	81.5	5.0	987	16	Q9RWP6	Q9rwp6 deinococcus
250	83.5	5.2	4074	4	Q86Z26	Q86z26 homo sapien	323	81.5	5.0	1467	10	Q9M033	Q9m033 arabidopsis
251	83	5.1	331	10	Q8LKN6	Q8lkn6 petunia hyb	324	81	5.0	265	2	Q9F7R6	Q9f7r6 gamma-prote
252	83	5.1	390	5	Q8IA36	Q8ia36 drosophila	325	81	5.0	265	10	Q8LQG9	Q8lqg9 oryza sativ
253	83	5.1	400	16	Q99SH3	Q99sh3 staphylococ	326	81	5.0	332	12	Q9PYL8	Q9pyl8 xestia c-ni
254	83	5.1	470	16	Q82VH7	Q82vh7 nitrosomona	327	81	5.0	381	16	Q9WZ94	Q9wz94 thermotoga
255	83	5.1	472	16	Q92BX9	Q92bx9 listeria in	328	81	5.0	382	5	Q9V5S3	Q9v5s3 drosophila
256	83	5.1	472	16	Q8Y7B0	Q8y7b0 listeria mo	329	81	5.0	413	16	Q8IAG8	Q8lag8 bacillus ce
257	83	5.1	479	11	Q9QWV7	Q9qwv7 mus musculu	330	81	5.0	438	16	Q8PF63	Q8pf63 xanthomonas
258	83	5.1	518	10	Q9QMBE5	Q9qmb5 lotus japon	331	81	5.0	503	5	Q9VAP6	Q9vap6 drosophila
259	83	5.1	818	11	Q9IY08	Q9ly08 mus musculu	332	81	5.0	629	16	Q92KY6	Q92ky6 rhizobium m
260	83	5.1	875	2	Q9RLA6	Q9rla6 rickettsia	333	81	5.0	653	5	Q95YJ5	Q95yj5 ciona intes
261	83	5.1	1021	10	Q7XKA2	Q7xka2 oryza sativ	334	81	5.0	858	5	Q9VGM0	Q9vgm0 drosophila
262	83	5.1	2096	16	Q7TWN7	Q7tnw7 mycobacteri	335	81	5.0	908	17	Q8Q0E6	Q8q0e6 methanosarc
263	83	5.1	3157	16	Q50378	Q50378 mycobacteri	336	81	5.0	1022	10	Q9LGK8	Q9lgk8 oryza sativ
264	82.5	5.1	343	17	Q97AH1	Q97ah1 thermoplasm	337	81	5.0	1234	5	Q7YXD0	Q7yxd0 caenorhabdi
265	82.5	5.1	422	16	Q92BT7	Q92bt7 listeria in	338	81	5.0	1520	5	Q7YSI0	Q7ysi0 caenorhabdi
266	82.5	5.1	511	16	Q9ZDL4	Q9zdl4 rickettsia	339	81	5.0	1549	5	Q8MM94	Q8mm94 caenorhabdi
267	82.5	5.1	562	16	P71654	P71654 mycobacteri	340	81	5.0	1583	5	Q8MLZ1	Q8mlz1 caenorhabdi
268	82.5	5.1	562	16	Q7TXU8	Q7txu8 mycobacteri	341	81	5.0	1583	5	Q8MV03	Q8mv03 caenorhabdi
269	82.5	5.1	579	16	Q835Z6	Q835z6 enterococcu	342	81	5.0	1654	5	Q7YSI9	Q7ysi9 caenorhabdi
270	82.5	5.1	601	16	Q830Z1	Q830z1 enterococcu	343	81	5.0	2078	5	P91834	P91834 caenorhabdi
271	82.5	5.1	875	2	Q9RLA9	Q9rla9 rickettsia	344	81	5.0	2847	4	O15018	O15018 homo sapien
272	82.5	5.1	898	10	Q9SIB9	Q9sib9 arabidopsis	345	80.5	5.0	234	10	Q94K08	Q94k08 arabidopsis
273	82.5	5.1	990	10	Q8L784	Q8l784 arabidopsis	346	80.5	5.0	281	16	Q92GG5	Q92gg5 rickettsia
274	82.5	5.1	2105	12	Q68772	Q68772 simian hemo	347	80.5	5.0	282	16	Q8XZX2	Q8xxz2 ralstonia s
275	82.5	5.1	2264	5	Q8I2E3	Q8i2e3 plasmodium	348	80.5	5.0	349	11	Q80W86	Q80w86 mus musculu
276	82	5.1	206	5	Q9N418	Q9n418 caenorhabdi	349	80.5	5.0	370	17	Q8TWI4	Q8twi4 methanopyru
277	82	5.1	322	16	Q9PC38	Q9pc38 xylella fas	350	80.5	5.0	383	10	Q41634	Q41634 umbellulari
278	82	5.1	398	5	Q8MS90	Q8ms90 drosophila	351	80.5	5.0	395	16	Q9RVT4	Q9rvt4 deinococcus
279	82	5.1	505	4	Q8TBP8	Q8tbp8 homo sapien	352	80.5	5.0	416	10	Q9FTS2	Q9fts2 oryza sativ
280	82	5.1	511	13	Q7ZXP7	Q7zxp7 xenopus lae	353	80.5	5.0	419	16	Q7WNM7	Q7wnm7 bordetella
281	82	5.1	526	16	Q8FTE3	Q8fte3 corynebacte	354	80.5	5.0	489	16	Q89I29	Q89iz9 bradyrhizob
282	82	5.1	539	16	Q8NLL9	Q8nll9 corynebacte	355	80.5	5.0	491	16	Q8YG44	Q8yg44 brucella me
283	82	5.1	543	16	Q9CM05	Q9cm05 pasteurella	356	80.5	5.0	516	6	Q8SQ69	Q8sq69 sus scrofa
284	82	5.1	548	11	Q80TG4	Q80tg4 mus musculu	357	80.5	5.0	521	5	Q8ISX7	Q8isx7 drosophila
285	82	5.1	554	16	Q7WDJ5	Q7wdj5 bordetella	358	80.5	5.0	567	12	Q8V526	Q8v526 monkeypox v
286	82	5.1	554	16	Q7W2K1	Q7w2k1 bordetella	359	80.5	5.0	847	3	Q7Z8L6	Q7z8l6 cochlicobolu
287	82	5.1	563	16	Q7VSD6	Q7vsd6 bordetella	360	80.5	5.0	898	10	Q84TR4	Q84tr4 lycopersico
288	82	5.1	602	11	Q8BWA1	Q8bwa1 mus musculu	361	80.5	5.0	1040	16	Q89DV7	Q89dv7 bradyrhizob
289	82	5.1	632	2	Q7X517	Q7x517 campylobact	362	80.5	5.0	1127	3	Q9P571	Q9p571 neurospora
290	82	5.1	658	11	Q8BUY6	Q8buy6 mus musculu	363	80.5	5.0	1307	11	Q8CJC2	Q8cjc2 mus musculu
291	82	5.1	695	11	Q80U56	Q8ou56 mus musculu	364	80.5	5.0	1741	5	O46095	O46095 drosophila
292	82	5.1	739	16	Q826H9	Q826h9 streptomyce	365	80.5	5.0	3432	12	Q90297	Q90297 japanese en
293	82	5.1	869	16	Q8PMF6	Q8pmf6 xanthomonas	366	80	4.9	201	10	Q93Z46	Q93z46 arabidopsis
294	82	5.1	1054	11	Q8VCD7	Q8vcd7 mus musculu	367	80	4.9	250	10	Q9T0A4	Q9t0a4 arabidopsis
295	82	5.1	1098	11	Q9WTN8	Q9wtm8 rattus norv	368	80	4.9	333	16	O87746	O87746 enterococcu
296	82	5.1	1100	4	Q94877	Q94877 homo sapien	369	80	4.9	373	2	Q9ZGC0	Q9zgc0 streptomyce
297	82	5.1	1392	12	Q9QTC5	Q9qtc5 marek's dis	370	80	4.9	397	17	Q9Y8Q8	Q9y8q8 aeropyrum p
298	82	5.1	1458	5	Q08095	Q08095 tripneustes	371	80	4.9	399	16	Q8A3L8	Q8a3l8 bacteroides
299	82	5.1	1991	2	Q83VG6	Q83vg6 erysipeloth	372	80	4.9	413	13	Q9YI37	Q9yi37 columba liv
300	81.5	5.0	240	16	Q815X3	Q815x3 bacillus ce	373	80	4.9	430	16	Q88GV4	Q88gv4 pseudomonas
301	81.5	5.0	331	16	Q8ZML1	Q8zml1 salmonella	374	80	4.9	430	16	Q7U3T1	Q7u3t1 synechococc
302	81.5	5.0	332	2	Q9ZAE0	Q9zae0 lactococcus	375	80	4.9	431	2	Q9RMU1	Q9rmul klebsiella
303	81.5	5.0	355	17	Q8PWP9	Q8pwp9 methanosarc	376	80	4.9	526	16	Q8ZQN2	Q8zqn2 salmonella
304	81.5	5.0	394	9	Q8SD91	Q8sd91 pseudomonas	377	80	4.9	535	11	Q80UW0	Q80uw0 mus musculu
305	81.5	5.0	395	2	Q8GA09	Q8ga09 escherichia	378	80	4.9	548	17	Q8TR30	Q8tr30 methanosarc
306	81.5	5.0	511	11	Q9WUV7	Q9wuv7 rattus norv	379	80	4.9	869	10	Q94GG1	Q94gg1 oryza sativ
307	81.5	5.0	519	11	Q91VZ1	Q91vz1 mus musculu	380	80	4.9	981	16	Q89S67	Q89s67 bradyrhizob
308	81.5	5.0	525	16	Q9JXJ7	Q9jxj7 neisseria m	381	80	4.9	1008	5	Q8MR76	Q8mr76 drosophila



382	80	4.9	1346	3	Q871M6	Q871m6 neurospora	455	78.5	4.9	368	10	Q9LSR0	Q9lsr0 arabidopsis
383	80	4.9	1384	16	Q7USX6	Q7usx6 rhodopirell	456	78.5	4.9	374	17	Q8TXL3	Q8txl3 methanopyru
384	80	4.9	1813	10	Q9ZSC9	Q9zsc9 lactuca sat	457	78.5	4.9	388	2	Q32633	Q32633 helicobacte
385	80	4.9	2268	5	Q8I4N5	Q8i4n5 plasmodium	458	78.5	4.9	427	2	Q9S1L6	Q9s1l6 streptover
386	80	4.9	2799	4	Q8I2F6	Q8izf6 homo sapien	459	78.5	4.9	441	10	Q84LL3	Q84ll3 zea mays su
387	79.5	4.9	274	2	Q87974	Q87974 bordetella	460	78.5	4.9	477	2	Q8L2C3	Q8l2c3 proteus vul
388	79.5	4.9	276	16	Q9RTL4	Q9rtl4 deinococcus	461	78.5	4.9	479	16	Q827M7	Q827m7 streptomyce
389	79.5	4.9	311	4	Q8IVJ4	Q8ivj4 homo sapien	462	78.5	4.9	481	16	Q7UV77	Q7uv77 rhodopirell
390	79.5	4.9	312	16	Q7W267	Q7w267 bordetella	463	78.5	4.9	523	16	Q9ZN39	Q9zn39 helicobacte
391	79.5	4.9	333	2	Q83007	Q83007 aeromonas p	464	78.5	4.9	529	16	Q92JT2	Q92jt2 rhizobium m
392	79.5	4.9	364	2	Q9LCB3	Q9lcb3 streptomyce	465	78.5	4.9	534	10	Q9FNI7	Q9fni7 arabidopsis
393	79.5	4.9	367	5	Q7YUQ8	Q7yuq8 trypanosoma	466	78.5	4.9	545	5	Q27620	Q27620 drosophila
394	79.5	4.9	379	2	Q8KXV8	Q8kxv8 shigella bo	467	78.5	4.9	550	11	Q8VCI0	Q8vcio mus musculu
395	79.5	4.9	386	16	Q89EF9	Q89ef9 bradyrhizob	468	78.5	4.9	550	11	Q9DLS0	Q9dis0 mus musculu
396	79.5	4.9	397	16	Q50518	Q50518 streptomyce	469	78.5	4.9	559	10	Q7XJE8	Q7xje8 prunus dulc
397	79.5	4.9	416	16	Q97IS5	Q97is5 clostridium	470	78.5	4.9	604	17	Q9VON3	Q9von3 pyrococcus
398	79.5	4.9	425	16	Q7V9T2	Q7v9t2 prochloroco	471	78.5	4.9	608	16	Q8ZND9	Q8znd9 salmonella
399	79.5	4.9	445	4	Q96M27	Q96m27 homo sapien	472	78.5	4.9	608	16	Q8Z523	Q8z523 salmonella
400	79.5	4.9	462	4	Q8IVL4	Q8ivl4 homo sapien	473	78.5	4.9	656	11	Q8CEI8	Q8cei8 mus musculu
401	79.5	4.9	464	4	Q86Y42	Q86y42 homo sapien	474	78.5	4.9	660	16	Q8E8N4	Q8e8n4 shewanella
402	79.5	4.9	484	16	Q8G729	Q8g729 bifidobacte	475	78.5	4.9	665	16	Q97K46	Q97k46 clostridium
403	79.5	4.9	545	17	Q980U2	Q980u2 sulfolobus	476	78.5	4.9	674	16	Q9KQD3	Q9kdq3 bacillus ha
404	79.5	4.9	548	2	Q9RMJ3	Q9rmj3 neisseria g	477	78.5	4.9	691	5	Q95Z95	Q95z95 leishmania
405	79.5	4.9	570	10	Q84P22	Q84p22 arabidopsis	478	78.5	4.9	715	10	Q9FYT6	Q9fyt6 zea mays (m
406	79.5	4.9	694	2	Q9Z187	Q9zi87 bacillus st	479	78.5	4.9	776	16	Q9QT18	Q9qt18 bradyrhizob
407	79.5	4.9	783	11	Q8BG83	Q8bg83 mus musculu	480	78.5	4.9	804	10	Q9SHM4	Q9shh4 arabidopsis
408	79.5	4.9	788	5	Q9VGL9	Q9vgl9 drosophila	481	78.5	4.9	848	16	Q9CHQ5	Q9chq5 lactococcus
409	79.5	4.9	805	11	Q8C842	Q8c842 mus musculu	482	78.5	4.9	890	10	Q9LJS0	Q9ljs0 arabidopsis
410	79.5	4.9	877	16	Q8XSY7	Q8xsy7 ralstonia s	483	78.5	4.9	909	16	Q8R6Z3	Q8r6z3 thermoanaer
411	79.5	4.9	898	10	Q84NF5	Q84nf5 lycopersico	484	78.5	4.9	917	5	Q8T9A1	Q8t9a1 drosophila
412	79.5	4.9	911	4	Q8IY66	Q8iy66 homo sapien	485	78.5	4.9	1005	11	Q8BLR5	Q8blr5 mus musculu
413	79.5	4.9	986	10	P93416	P93416 oryza sativ	486	78.5	4.9	1312	3	Q8WZV2	Q8wzv2 neurospora
414	79.5	4.9	988	10	Q64454	Q64454 oryza sativ	487	78.5	4.9	1654	16	Q8YV86	Q8yv86 anabaena sp
415	79.5	4.9	1072	16	Q9CF64	Q9cf64 lactococcus	488	78.5	4.9	2124	16	Q98M03	Q98m03 rhizobium l
416	79.5	4.9	1179	4	Q60271	Q60271 homo sapien	489	78.5	4.9	3424	5	Q9VT22	Q9vt22 drosophila
417	79.5	4.9	1204	15	Q7ZKZ9	Q7zkz9 recombinant	490	78.5	4.9	3479	5	Q9GPT8	Q9gpt8 drosophila
418	79.5	4.9	1257	10	Q64516	Q64516 arabidopsis	491	78.5	4.9	3479	5	Q9VT28	Q9vt28 drosophila
419	79.5	4.9	1311	4	Q8IZX7	Q8izx7 homo sapien	492	78	4.8	115	11	Q80VW6	Q80vw6 mus musculu
420	79.5	4.9	1506	5	Q7YU30	Q7yu30 drosophila	493	78	4.8	173	11	Q99M72	Q99m72 mus musculu
421	79.5	4.9	1520	5	Q86B63	Q86b63 drosophila	494	78	4.8	242	16	Q8Y8M0	Q8y8m0 listeria mo
422	79.5	4.9	2535	10	Q8I018	Q8i018 arabidopsis	495	78	4.8	293	16	Q7TVE2	Q7tve2 mycobacteri
423	79	4.9	247	16	Q8Z922	Q8z922 salmonella	496	78	4.8	293	17	Q8ZWL6	Q8zw16 pyrobaculum
424	79	4.9	354	2	Q8KQ27	Q8kq27 streptomyce	497	78	4.8	304	13	Q7ZYH0	Q7zyh0 xenopus lae
425	79	4.9	372	10	Q80512	Q80512 arabidopsis	498	78	4.8	313	16	Q7V0G9	Q7v0g9 prochloroco
426	79	4.9	410	16	Q05446	Q05446 mycobacteri	499	78	4.8	328	16	Q9KYM8	Q9kym8 streptomyce
427	79	4.9	451	13	Q7ZTV9	Q7ztv9 brachydanio	500	78	4.8	336	17	Q9HPL0	Q9hpl0 halobacteri
428	79	4.9	504	16	Q89XV7	Q89xv7 bradyrhizob							
429	79	4.9	506	13	Q9PVI1	Q9pvi1 fundulus he							
430	79	4.9	514	2	Q8KY23	Q8ky23 uncultured							
431	79	4.9	531	5	Q8T8Q4	Q8t8q4 drosophila							
432	79	4.9	540	10	Q9FL17	Q9fl17 arabidopsis							
433	79	4.9	562	16	Q88KJ7	Q88kj7 pseudomonas							
434	79	4.9	571	16	Q8KBC7	Q8kbc7 chlorobium							
435	79	4.9	588	2	Q69007	Q69007 thermus sp.							
436	79	4.9	610	17	Q97V19	Q97v19 sulfolobus							
437	79	4.9	632	17	Q29794	Q29794 archaeoglob							
438	79	4.9	720	10	Q941N7	Q941n7 phytophthor							
439	79	4.9	758	16	Q7UUY1	Q7uuy1 rhodopirell							
440	79	4.9	900	10	Q93VK2	Q93vk2 phytophthor							
441	79	4.9	900	10	Q941N6	Q941n6 phytophthor							
442	79	4.9	907	10	Q9S236	Q9s236 arabidopsis							
443	79	4.9	995	10	Q94A28	Q94a28 arabidopsis							
444	79	4.9	1090	16	Q8P6S5	Q8p6s5 xanthomonas							
445	79	4.9	1207	11	Q8BKF1	Q8bkf1 mus musculu							
446	79	4.9	1207	11	Q8BJE0	Q8bje0 mus musculu							
447	79	4.9	2749	10	Q8SA93	Q8sa93 zea mays (m							
448	78.5	4.9	224	10	Q84LL2	Q84ll2 zea mays su							
449	78.5	4.9	270	16	Q8RGJ9	Q8rgj9 fusobacteri							
450	78.5	4.9	293	16	Q8NY90	Q8ny90 staphylococ							
451	78.5	4.9	314	16	Q07521	Q07521 bacillus su							
452	78.5	4.9	342	16	Q7UVH8	Q7uvh8 rhodopirell							
453	78.5	4.9	355	3	Q7ZA39	Q7za39 emericeella							
454	78.5	4.9	361	17	Q974W0	Q974w0 sulfolobus							

ALIGNMENTS

RESULT 1  
Q8NCCC9  
ID Q8NCCC9 PRELIMINARY; PRT; 975 AA.  
AC Q8NCCC9;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein FLJ90334.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,  
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,  
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,  
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;  
RT "NEDO human cDNA sequencing project."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK074875; BAC11227.1; -.







Query Match 36.5%; Score 590; DB 10; Length 897;  
Best Local Similarity 40.6%; Pred. No. 5e-44;  
Matches 119; Conservative 56; Mismatches 108; Indels 10; Gaps 3;

QY 8 FATCCVAIEVLGIAVFLRGFFPA-PVRSSARAEGHGAEPPEPSAGASSNWTTLPPPLFS 66  
Db 14 FTVAGILLQIIIGLSIFVGFPPVPKPTLSGVSGSESYRDPFCDSS--LISNESELHHPEKL 71

QY 67 KVVIVLIDALRDDDFVFGSKG-----VKFMPYTTYLVVEKGASHSFVAEAKPPTVMPRI 119  
Db 72 RLLYQVIDGLPAEFVLGDKGPKPEKVKLVKESMPYTSLLANGDAIGYHAKAAPPTVMPRL 131

QY 120 KALMTGSLPGFVDVIRNLNSPALLEDSDVIRQAKAAGKRIVFYGDETWVKLFPKHVEYDVG 179  
Db 132 KAMVSGAIGGFLDVAFNFTQALLDDNLLILHYLGLDHVCHTGGGRNSPLMPAKLKEM 191

QY 180 TTTSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIGHISGPNPLIGQKLSEM 239  
Db 192 VSSFFVXDVTQVDRNVSRHLPDELNSDDWNLLILHYLGLDHVCHTGGGRNSPLMPAKLKEM 251

QY 240 DSVLMKIHTSLQSKERETPLPLNLLVCGDHGMSSETGSHGASSTEEVNTPLILI 292  
Db 252 DDIVRTWHLRAMWDRSHDQGTLLIIVSDHGMTENGHNHGGSSYEETDSLMLFI 304

RESULT 7  
Q8TGB2  
ID Q8TGB2 PRELIMINARY; PRT; 892 AA.

AC Q8TGB2;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Putative Gpi7p.  
GN GPI7.

OS Candida albicans (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5476;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SC5314;  
RA Richard M., Ibata-Ombetta S., Dromer F., Bordon-Pallier F.,  
RA Jouault T., Gaillardin C.;  
RT "Complete Glycosylphosphatidylinositol Anchors are Required in Candida  
RT albicans for Full Morphogenesis, Virulence and Resistance to  
RT Macrophages";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF348498; AAL83897.1; --  
SQ SEQUENCE 892 AA; 101554 MW; BF04A57E0356C247 CRC64;

Query Match 36.1%; Score 583; DB 3; Length 892;  
Best Local Similarity 42.6%; Pred. No. 2.1e-43;  
Matches 127; Conservative 46; Mismatches 91; Indels 34; Gaps 8;

QY 15 IEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTLP-----PPLFSKV 68  
Db 18 INIIGFLVFLRGFFPSKV-----VLPGFNSFQDSTKSPFSDHYGTPQFNKF 63

QY 69 VIVLIDALRDDDFVFGSKGVKFMPTTYLVVEKGASHSFVAEAKPPTVMPRIKALMTGSLP 128  
Db 64 ILMVVDAMRSDFCFSDR--SNFSFLHQLINQGHALPFTAFSNPPTVTLPRKGITTGTP 121

QY 129 GFVDVIRNL-----NSPAL-LEDSVIRQAK-AAGKRIVFYGDETWVKLFPKHVEYDGTT 181  
Db 122 NFLDAILNVADDQDSDQGLHNQDSVWHQFRHSNNKNTINFFGDDTWLKLFDQDTEFEGTN 181

QY 182 SFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIGHISGPNPLIGQKLSEMDS 241  
Db 182 SFFVSDYTEVDNNVTRHLDQSSNKNKWDGLILHYLGLDHIGHKGGPESPYMKPKQIEMDK 241

QY 242 VLMKIHTSLQSKERETPLPLNLLVCGDHGMSSETGSHGASSTEEVNTPLILISSAFERK 299  
Db 242 ILQRLYTYV-TKNDDT----LIVMGDHGMNEIGHGSSPGETSAAALSFIKPFNHNK 294

RESULT 8  
Q19870  
ID Q19870 PRELIMINARY; PRT; 795 AA.

AC Q19870;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE F28C6.4 protein.  
GN F28C6.4.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Burton J.;  
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
RT investigating biology";  
RL Science 282:2012-2018(1998).  
DR EMBL; Z68315; CAA92675.1; --  
DR PIR; T21487; T21487.  
DR WormPep; F28C6.4; CE03275.  
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000169; SHprot acsite.  
DR PROSITE; PS00639; THIOLEPROTEASE\_HIS; 1.  
SQ SEQUENCE 795 AA; 90480 MW; 1D7C4C3ADECE7B13 CRC64;

Query Match 32.4%; Score 524; DB 5; Length 795;  
Best Local Similarity 42.4%; Pred. No. 3.7e-38;  
Matches 108; Conservative 51; Mismatches 80; Indels 16; Gaps 5;

QY 67 KVVIVLIDALRDDDFVFGSKGVKFMPTTYLVVEKGASHSFVAEAKPPTVMPRIKALMTGS 126  
Db 104 RLVMFVIDAFRLSELTSSKSP--MSFTKSEITKSAKLFDAYARMPVTILPRITAYLTGT 161

QY 127 LPGFVDVIRNLNSPALLEDSDVIRQAKAAGKRIVFYGDETWVKLFPKHVEYDGTTSFFVS 186  
Db 162 LPSFGTVLTNLATAEMKTANWISRIQKIGKVHFFGDDTWIRLLPRSFKEFGVTSFFVS 221

QY 187 DYTEVDNNVTRHLDKVLKRGD--WDILILHYLGLDHIGHISGPNPLIGQKLSEMDSVLM 244  
Db 222 DYTVDNNVTRHLDTELSNTNHSWDALILHYLGLDHIGHSLGGSSKIPEKLEKEMDDVIG 281

QY 245 KIHTSLQSKERETPLPLNLLVCGDHGMSSETGSHGASSTEEVNTPLILISSAFERKPGD-- 302  
Db 282 RIHKYLLKS-STSVDDQESYLIVCGDHGHTAAGSHGGASPDETRVPVVIWK--FGREEGNKN 338

QY 303 -----IRHPKHVQ 310  
Db 339 YGNQDDSLKQPPRIE 353

RESULT 9  
Q9V4N0  
ID Q9V4N0 PRELIMINARY; PRT; 927 AA.

AC Q9V4N0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CG2144 protein.  
GN CG2144.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.



OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,  
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RT "Sequencing of *Drosophila melanogaster* genome.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochnick S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
RT "Annotation of *Drosophila melanogaster* genome.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.

RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003840; AAF59237.3; -  
DR FlyBase; FBgn0033187; CG2144.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000508; Peptidase S26.  
DR PROSITE; PS00761; SPASE I.3; 1.  
SQ SEQUENCE 927 AA; 104588 MW; 1A543894BBAD7EF5 CRC64;  
  
Query Match 31.6%; Score 511.5; DB 5; Length 927;  
Best Local Similarity 41.1%; Pred. No. 6.2e-37;  
Matches 118; Conservative 43; Mismatches 99; Indels 27; Gaps 9;  
  
QY 19 GIAVFLRGFFPAPVRSSARAEHGAEPAPPEPSAGASSNWTTLPPLFESKVIVLIDALRD 78  
Db 21 GAVLFLIGFFPA--SYSVAEKESTVPEGRPTALLGMELTP-PPPAYDSFVLLVLDALRD 76  
  
QY 79 DFVFGSKGVKFMPTT-TYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGFVDVIRNL 137  
Db 77 DFPDATS---MPVAYSRACEKLLKLVHVDI-----PTVTMPRLKSITTTGSLNFIDIALNV 127  
  
QY 138 NSPALLEDVIRQAKAAGKRIYFYGDETWKLFPPKHFV-EYDGTTSFFVSDYTEVDNNVT 196  
Db 128 GHTEQMQDSFLHRLKQNRVVSFAGDHTWVKLFPSEFTRQVENHDSFYVNDYEGDRNVT 187  
  
QY 197 RHLDKVLKRGDWDILILHYLGLDHIHISGPNISPLIGOKLSEMDSVLMKI--HTSLQSK 254  
Db 188 KTELELERSDWSLLILHYLGLDHIHISGPNISPLIGOKLSEMDSVLMKI--HTSLQSK 242  
  
QY 255 RETPLPN-LLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db 243 ---FPNVLLMLTGDHGMADGGHGGTGAETPLVPLVLYNNCSKTP 285  
  
RESULT 10  
Q9GM09 PRELIMINARY; PRT; 333 AA.  
ID Q9GM09  
AC Q9GM09  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheidae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
libraries.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB050262; BAB17014.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 333 AA; 37237 MW; 1D2EB0459ACCE97C CRC64;  
  
Query Match 31.6%; Score 511; DB 6; Length 333;  
Best Local Similarity 97.0%; Pred. No. 1.5e-37;  
Matches 98; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 210 ILILHYLGLDHIHISGPNISPLIGOKLSEMDSVLMKIHTSLQSKERETPLNLLVLCGDH 269  
Db 1 MLILHYLGLDHIHISGPNISPLIGOKLSEMDSVLMKIHTSLQSKERETPLNLLVLCGDH 60

QY 270 GMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ 310  
Db 61 GMSETGSHGASSMEEVNTPLILISSAFERKPGDIRHPKHVQ 101

RESULT 11  
Q8LNL1 PRELIMINARY; PRT; 692 AA.

AC Q8LNL1  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative protein similar to phosphatidylinositol glycan (Hypothetical protein).  
DE OSJNBA0071120.7.  
GN Oryza sativa (japonica cultivar-group).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA McCombie W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,  
RA Kuit K., Nascimento L., Zutavern T., Baliya V., Bell M., Baker J.,  
RA Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,  
RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;  
RA "Genomic sequence for Oryza sativa, Nipponbare strain, clone  
RT OSJNBA0071120, from chromosome 10, complete sequence."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA The Rice Chromosome 10 Sequencing Consortium;  
RA "In-depth view of structure, activity, and evolution of rice  
RT chromosome 10."  
RL Science 300:1566-1569(2003).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;  
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC074355; AAM74245.1; -  
DR EMBL; AE017062; AAP52339.1; -  
DR Gramene; Q8LNL1; -  
KW Hypothetical protein.  
SQ SEQUENCE 692 AA; 77188 MW; 20458C34AE632241 CRC64;

Query Match 29.1%; Score 471; DB 10; Length 692;  
Best Local Similarity 38.2%; Pred. No. 1.8e-33;  
Matches 108; Conservative 47; Mismatches 110; Indels 18; Gaps 5;

QY 18 LGIAVFLRGFFPAPVRSSARAEHGAEPPEPAPEPSAGASSNWTTLPPPLFSKVIVLIDALR 77  
Db 26 LAIYLFTRGFLLTRELDVHSHR-----DDRIGISPGCSSWPPPAVDRLVIVVLDALR 78

QY 78 DDFV----FGSKGVKFMPTTYLV-----EKGASHSFVAEAKPPTVTMPRIKALMTGSLP 128  
Db 79 FDFVAPSTFFQERQRPWMDKLOVLQRLAARAEKTSARIFKALADPPTTSLQRLKALTGGLP 138

QY 129 GFVDVIRNLNSPALLEDVIRQAKAGKRVFVGDETWVKLFPKHFEVDGTTTSFFVSDY 188  
Db 139 TFIDVGNISFGAPAIVEDNIMHQFAKNGKRVVMGDDTWIQLYPERHFNKSYPYPSFNVKDL 198

QY 189 TEVDNNVTRHLDKVLKRGDWDILILHYGLDHIHISGPNPLIGQKLSMDSVLMKIHT 248  
Db 199 DTVDNGVIEHLLPSLHKNDWDVLIHAFGLVDHAGHIFGVDSTPMIQLEQNRILEVDID 258

QY 249 SLQSKERE-TPLPN-LLVLCGDHGMSETGSHGASSTEEVNTPL 289  
Db 259 TLKSLSTSGGPHENTLLLVMGDHDGQTLNGDHHGGGTAEVETSL 301

RESULT 12  
Q7YU86 PRELIMINARY; PRT; 1077 AA.

AC Q7YU86  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE SD07983p.  
GN CG12263.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Celniker S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BT009934; AAQ22403.1; -  
SQ SEQUENCE 1077 AA; 121302 MW; 979E6F41AE45EABC CRC64;

Query Match 26.1%; Score 421.5; DB 5; Length 1077;  
Best Local Similarity 33.2%; Pred. No. 1e-28;  
Matches 99; Conservative 50; Mismatches 116; Indels 33; Gaps 7;

QY 19 GIAVFLRGFFPAPV--RSSARAEHGAEPPEAPE-----PSAGASSNWTTLPPPL 64  
Db 19 GVMFLSRGFLRLARVSKTETSTCRRLSTNPNAEVYVLTDEVVNEIFKDVNASSN---LCLPQ 75

QY 65 FSKVIVLIDALRDDP-VFGSKGVKFMPTTYLV-----EKGASHFVA--EAKPPTVT 115  
Db 76 KSKVIVLVVDALKYEGLYRANATDPLPYENKLVVLQELLQONPDHARLMFRADPPTTT 135

QY 116 MPRIKALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAGKRVFVGDETWVKLFPKHV 175  
Db 136 LQRLKGLTGTSLPTFIDIGSNFASPEINEDNIQIVKNDLPVVFGLDSTWTDLYPRRFK 195

QY 176 EYDGTTSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYGLDHIHISGPNPLIGQK 235  
Db 196 RSYSPSFDIFDLDSDVNEILKHLPKLESKDQWQVLAHFLGVDHCGHKHGMHEEMARK 255

QY 236 LSEMDSVLMKIHTSLOSKEKETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILIS 293  
Db 256 LGMNEVIRSVVAMDN-----DTLLVMGDHGMTASGDHGGDTTDETNALLFAYS 306

RESULT 13  
Q9V8H8 PRELIMINARY; PRT; 1077 AA.

AC Q9V8H8  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CG12263 protein.  
GN CG12263.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkely;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-pfannkuch C., Baldwin D.,  
 RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,  
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of Drosophila melanogaster";  
 RT Science 287:2185-2195(2000).  
 RL EMBL; AE003799; AAF57689.1; --  
 DR FlyBase; FBgn0034346; CG12263.  
 DR GO; GO:0016787; P:hydrolyase activity; IEA.  
 DR GO; GO:0009117; P:nucleotide metabolism; IEA.  
 DR InterPro; IPR002591; Phosphodiester.  
 DR Pfam; PF01663; Phosphodiester; 1.  
 SQ SEQUENCE 1077 AA; 121329 MW; 9EE894B0F2E243F5 CRC64;

Query Match 25.9%; Score 418.5; DB 5; Length 1077;  
 Best Local Similarity 33.2%; Pred. No. 1.9e-28;  
 Matches 99; Conservative 49; Mismatches 117; Indels 33; Gaps 7;

QY 19 GIAVFLRGFFPAPV---RSSARAEHGAEPPE-----PSAGASSNWTLPPL 64  
 DB 19 GVMFLSRGFLARVSKTETSTCRRLSTNPNAEYVLTDEVVNEIFKDVNASSN---LCLPQ 75  
 QY 65 FSKVIVLIDALRDDF-VFSGKGVKMPYTYLV-----EKGASHSFA--EAKPPTVT 115  
 DB 76 KSKVIVLVVDALKYEFGLYRANATDPLPYENKLVVLQELLQONPDHARLMFRADPPTTT 135  
 QY 116 MPRIKALMTGSLPGFVDVIRNLNSPALLEDSDVIRQAKAAGRIYFYGDETVVKLFEPKHFV 175  
 DB 136 LQRLKGLTGTSLPTTFIDIGSNFASPEINEDNIIDQIVKNDLPVFLGDSWTDLPHRFK 195  
 QY 176 EYDGTTSFFVSDYTEVDNVTNRHLDKVLRGWDILHLGLDHIHSGPNSPLIGQK 235  
 DB 196 RSYSPSPDFIDFLDSVDNEILKLPKELESQWQVLAHFLGVDHCGHKHGMHEEMARK 255  
 QY 236 LSEMDSVLMKIHTSLOSKEKETPLNLLVLCGDMGSETGSHGASSTEEVNTPLILIS 293  
 DB 256 LGEMNEVIRSVVAAADN-----DTLLVMGDHGMWGTASGDHGGDTTDETNALLFAYS 306

RESULT 14  
 Q9FFI6  
 ID Q9FFI6 PRELIMINARY; PRT; 884 AA.  
 AC Q9FFI6;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE Genomic DNA, Chromosome 5, Pl clone:MKP11.  
 OS Arabidopsis thaliana (Mouse-ear cross).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RX MEDLINE=97471969; PubMed=9330910;  
 RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,  
 RA Miyajima N., Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence  
 RT features of the 1.6 Mb regions covered by twenty physically assigned  
 RT pl clones."  
 RL DNA Res. 4:215-230(1997).  
 DR EMBL; AB005238; BAB10512.1; --  
 SQ SEQUENCE 884 AA; 97926 MW; 0E247D729AC8BE0A CRC64;

Query Match 25.7%; Score 415.5; DB 10; Length 884;  
 Best Local Similarity 33.9%; Pred. No. 2.6e-28;  
 Matches 97; Conservative 46; Mismatches 114; Indels 29; Gaps 5;

QY 15 IEVLGIAVFLRGFF---PAPVRSSARAEHGAEPPEPSAGASSNWTLPPLPSKVVI 70  
 DB 18 IHAIAILIFTRGFLLRTELFFHSTC-SDVLSPLCLASPRSNHDS--SSEPKPMWDKLT 74  
 QY 71 VLIDALRDDFVFGSKGVKMPYTYLVLRGASHSFVAEAKPPTVTMPRIKALMTGSLPGF 130  
 DB 75 LQTLAFAND-----SSAKIFKAFADPPTTSLQRLKGLTGTGLPTF 114  
 QY 131 VDVIRNLNSPALLEDSDVIRQAKAAGRIYFYGDETVVKLFEPKHFVEYDGTSPFVSDYTE 190  
 DB 115 IDIGNSFGAPAIVEDNFQNLVLRGKRLVMGDDTWTQLFPNQFQKSPFSPNVKDLDT 174  
 QY 191 VDNVTRHLDKVLRGWDILHLGLDHIHSGPNSPLIGKLSMDSVLMKIHTSL 250  
 DB 175 VDNGCIEHLFPTLFKDDVDVLAHFLGVDHAGHIFGVDSPPMINKLEQYNSVLEKVINIL 234  
 QY 251 QSKERETPL--PNLLVLCGDMGSETGSHGASSTEEVNTPLILISS 294  
 DB 235 ESQAGPGGLHENTMLIVMGHGQTLNGDHGGTAEEVETTMFAMST 280

RESULT 15  
 O13663  
 ID O13663 PRELIMINARY; PRT; 918 AA.  
 AC O13663;  
 DT 01-JAN-1998 (Tremblrel. 05, Created)  
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE ORF YLL031C.  
 GN PI072 OR SPBC27B12.06.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972H-;  
 RA Kushida N., Yamazaki S., Tanaka T., Jinno K., Haikawa Y., Yamazaki J.,  
 RA Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,  
 RA Ogura K., Otsuka R., Kudoh Y., Yanagida M., Machida M., Zhang M.Q.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972H-;  
 RA Wood V., Rajandream M.A., Barrell B.G., Lauber J., Hilbert H.,  
 RA Duesterhoeft A.;  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB004539; BAA21454.1; --



Search completed: August 2, 2004, 16:29:56  
Job time : 53 secs



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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:25:48 ; Search time 13 Seconds  
(without alignments)  
1241.673 Million cell updates/sec

Title: US-10-036-150-45  
Perfect score: 1617  
Sequence: 1 MRLGSGTFATCCVAIEVLGI.....LISSAFERKPGDIRHPKHVQ 310

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	634.5	39.2	758	1 YA93_SCHPO	Q09782 schizosacch
2	508.5	31.4	830	1 YJG2_YEAST	P40367 saccharomyc
3	490	30.3	1093	1 PIGO_MOUSE	Q9jj16 mus musculu
4	481	29.7	1088	1 PIGO_HUMAN	Q8teg8 homo sapien
5	170	10.5	919	1 YKQ5_YEAST	P36051 saccharomyc
6	114	7.1	963	1 IRE2_RAT	Q62751 rattus norv
7	111.5	6.9	906	1 NPP1_MOUSE	P06802 m ectonucle
8	111	6.9	885	1 NPP2_RAT	Q64610 r ectonucle
9	109	6.7	906	1 SKS1_ARATH	Q8vxx5 arabidopsis
10	108.5	6.7	906	1 NPP1_ARATH	Q924c3 r ectonucle
11	107	6.6	875	1 NPP3_HUMAN	Q14638 h ectonucle
12	105.5	6.5	863	1 NPP2_HUMAN	Q13822 h ectonucle
13	101.5	6.3	862	1 NPP2_MOUSE	Q9rie6 m ectonucle
14	101	6.2	925	1 NPP1_HUMAN	P22413 h ectonucle
15	98.5	6.1	502	1 GPM1_MYCPE	Q8ew33 mycoplasma
16	97.5	6.0	742	1 YCR6_YEAST	P25353 saccharomyc
17	96.5	6.0	2109	1 RRPL_VSVSJ	P03523 vesicular s
18	95.5	5.9	513	1 P2BC_MOUSE	P48455 mus musculu
19	95	5.9	818	1 CDB1_HUMAN	Q9v5f3 homo sapien
20	94.5	5.8	388	1 TRB1_PYRAB	Q9v198 pyrococcus
21	94	5.8	388	1 TRB1_PYRFU	Q8u093 pyrococcus
22	92.5	5.7	650	1 GHR_MOUSE	P16882 mus musculu
23	92	5.7	638	1 GHR_RAT	P16310 rattus norv
24	90.5	5.6	963	1 IRE2_HUMAN	P48200 homo sapien
25	90	5.6	634	1 GHR_SHEEP	Q28575 ovis aries
26	89.5	5.5	465	1 COBQ_ACICA	Q43989 acinetobact
27	89.5	5.5	510	1 GPM1_ANTSP	Q06464 antithamnio
28	89	5.5	359	1 UNG_YEAST	P12887 saccharomyc
29	88.5	5.5	258	1 HIS6_ECOL6	Q8fg48 escherichia
30	88.5	5.5	258	1 HIS6_ECOLI	P10373 escherichia
31	88.5	5.5	642	1 KF12_MOUSE	Q9d2z8 mus musculu
32	88	5.4	525	1 Y3J7_METAC	Q8ti22 methanosarc
33	88	5.4	875	1 NPP3_RAT	P97675 r ectonucle



107	79	4.9	368	1	ALR_LISIN	Q92dc9	listeria in	180	76	4.7	470	1	FUCK_HAEIN	P44399	haemophilus
108	79	4.9	416	1	ALAT_BOVIN	P34955	bos taurus	181	76	4.7	471	1	LEU2_CHRVO	Q7nub6	chromobacte
109	79	4.9	427	1	DSL1_CHICK	P34822	gallus gall	182	76	4.7	493	1	YEB6_YEAST	P39997	saccharomyc
110	79	4.9	510	1	GPML_BACST	Q9x519	bacillus st	183	76	4.7	510	1	GPML_BACSU	P39773	bacillus su
111	79	4.9	637	1	DNAK_BUCAI	O32464	buchnera ap	184	76	4.7	638	1	GHR_RABIT	P19941	oryctolagus
112	79	4.9	638	1	GHR_PIG	P19756	sus scrofa	185	76	4.7	805	1	VPH1_SCHPO	O13742	schizosacch
113	78.5	4.9	409	1	DEOB_BUCAP	Q8k936	buchnera ap	186	76	4.7	831	1	PRLR_MELGA	Q91094	meleagris g
114	78.5	4.9	501	1	PDIL_ARATH	Q9xi01	arabidopsis	187	76	4.7	851	1	MUTS_STRP8	Q8nz24	streptococc
115	78.5	4.9	559	1	MDL1_PRUDU	O24243	prunus dulc	188	76	4.7	851	1	YDBG_SCHPO	Q10366	schizosacch
116	78.5	4.9	582	1	SYN2_HUMAN	Q92777	homo sapien	189	76	4.7	908	1	ACON_BACSU	P09339	bacillus su
117	78.5	4.9	600	1	DSBD_VIBCH	Q9knn1	vibrio chol	190	76	4.7	956	1	PODK_FLAPR	Q42736	flaveria pr
118	78.5	4.9	609	1	YL15_MYCLE	P46509	mycobacteri	191	76	4.7	1068	1	RBL1_HUMAN	P28749	homo sapien
119	78.5	4.9	656	1	PTPR_MOUSE	Q62132	mus musculu	192	76	4.7	1165	1	POL_GALV	P21414	gibbon ape
120	78.5	4.9	761	1	YA88_AQUAE	Q67178	aquifex aeo	193	76	4.7	2366	1	TOXB_CLODI	P18177	clostridium
121	78.5	4.9	773	1	Z341_HUMAN	Q9byn7	homo sapien	194	75.5	4.7	222	1	HIS5_STRCO	P16249	streptomyce
122	78.5	4.9	775	1	TREY_ARTSQ	Q44315	arthrobacte	195	75.5	4.7	238	1	LEXA_RHIME	Q92pw3	rhizobium m
123	78.5	4.9	1108	1	CYGE_RAT	P51840	rattus norv	196	75.5	4.7	312	1	LDH_MYCGB	P47698	mycoplasma
124	78.5	4.9	1216	1	PIB1_RAT	P10687	rattus norv	197	75.5	4.7	394	1	TRPB_BUCBP	P59458	buchnera ap
125	78.5	4.9	4911	1	MLL3_HUMAN	Q8nez4	homo sapien	198	75.5	4.7	466	1	LEU2_BUCTS	O31293	buchnera ap
126	78	4.8	330	1	CAHX_FLAPR	P46511	flaveria br	199	75.5	4.7	510	1	GPML_VIBPA	Q87kz5	vibrio para
127	78	4.8	437	1	E2F1_HUMAN	Q01094	homo sapien	200	75.5	4.7	512	1	GPML_CLOPE	Q8xku2	clostridium
128	78	4.8	485	1	GATA_BACST	Q04458	saccharomyc	201	75.5	4.7	512	1	PDI_MEDSA	P29828	medicago sa
129	78	4.8	532	1	YM00_YEAST	Q9hle7	thermoplas	202	75.5	4.7	567	1	VE06_VACCC	P21047	vaccinia vi
130	78	4.8	546	1	SYR_THEAC	Q9wwg9	pseudomonas	203	75.5	4.7	732	1	ELM2_MOUSE	Q8bh15	mus musculu
131	78	4.8	638	1	DNAK_PSESG	O32482	legionella	204	75.5	4.7	900	1	KDPD_CLOAB	P94608	clostridium
132	78	4.8	644	1	DNAK_LEGPN	Q09285	caenorhabdi	205	75.5	4.7	1102	1	CARB_STRCO	Q9kxr6	streptomyce
133	78	4.8	867	1	YQK1_CABEL	Q09285	caenorhabdi	206	75.5	4.7	2504	1	FAS_HUMAN	P49327	homo sapien
134	78	4.8	902	1	IF2_BRAJA	Q89wa9	bradyrhizob	207	75	4.6	142	1	RL11_BUCAI	P57150	buchnera ap
135	78	4.8	1010	1	PUR2_HUMAN	P22102	h trifuncti	208	75	4.6	249	1	SURE_CLOTE	Q899m5	clostridium
136	78	4.8	1019	1	VP3_RDVF	Q98630	rice dwarf	209	75	4.6	270	1	NAGB_BACTN	Q8a094	bacteroides
137	77.5	4.8	256	1	HIS6_PASMU	Q9clm0	pasteurella	210	75	4.6	367	1	FPPS_CHICK	P08836	gallus gall
138	77.5	4.8	394	1	DEOB_BACAA	Q8lme0	bacillus an	211	75	4.6	403	1	TRB1_METMA	Q8pt95	methanosarc
139	77.5	4.8	409	1	NER1_RAT	Q99pw3	rattus norv	212	75	4.6	407	1	DEOB_BUCAI	P57607	buchnera ap
140	77.5	4.8	451	1	RPA2_MEITH	O27126	methanobact	213	75	4.6	440	1	GAT4_RAT	P46152	rattus norv
141	77.5	4.8	503	1	SNAL_MOUSE	Q61234	mus musculu	214	75	4.6	466	1	HOB1_SCHPO	O74352	schizosacch
142	77.5	4.8	521	1	P2BA_BOVIN	P48452	bos taurus	215	75	4.6	469	1	LEU2_NEIMA	Q9ju82	neisseria m
143	77.5	4.8	521	1	P2BA_HUMAN	Q08209	homo sapien	216	75	4.6	469	1	LEU2_NEIMB	Q9jzi5	neisseria m
144	77.5	4.8	545	1	ESTB_DROMI	O16170	drosophila	217	75	4.6	485	1	SYE_AGR75	Q8u7h5	agrobacteri
145	77.5	4.8	545	1	ESTB_DROPS	P25726	vaccinia vi	218	75	4.6	536	1	YAGH_ECOLI	P77713	escherichia
146	77.5	4.8	567	1	VE06_VACCV	P21607	vaccinia vi	219	75	4.6	553	1	SYR_STAAM	Q932f6	staphylococ
147	77.5	4.8	579	1	Y359_CHLMU	Q9pkv2	chlamydia m	220	75	4.6	553	1	SYR_STAAN	Q99w05	staphylococ
148	77.5	4.8	609	1	YL15_MYCTU	O33250	mycobacteri	221	75	4.6	553	1	SYR_STAAN	Q8nxt8	staphylococ
149	77.5	4.8	656	1	PTPR_RAT	O08617	rattus norv	222	75	4.6	562	1	SYR_THETN	Q8r786	thermoanaer
150	77.5	4.8	801	1	SYFB_STRP3	Q8k820	streptococc	223	75	4.6	566	1	DCPY_EMENI	P87208	emericaella
151	77.5	4.8	1067	1	TRI1_STRCO	Q9rde2	streptomyce	224	75	4.6	711	1	SPE2_ARATH	O23141	arabidopsis
152	77	4.8	175	1	LPPN_MYCTU	Q50693	mycobacteri	225	75	4.6	922	1	DPO1_RICFE	Q9raa9	rickettsia
153	77	4.8	403	1	E2F1_CHICK	Q90977	gallus gall	226	75	4.6	976	1	EPA2_HUMAN	P29317	homo sapien
154	77	4.8	404	1	GAT5_MOUSE	P97489	mus musculu	227	75	4.6	1244	1	YP83_CAEEL	Q09441	caenorhabdi
155	77	4.8	528	1	NIEK_FRAAL	Q57118	frankia aln	228	75	4.6	1391	1	RPOB_MYCPN	P78013	mycoplasma
156	77	4.8	549	1	GYRA_MYCKA	Q49608	mycobacteri	229	75	4.6	3866	1	HRX_MOUSE	P55200	mus musculu
157	77	4.8	631	1	MX1_MOUSE	P09922	mus musculu	230	74.5	4.6	242	1	NAGB_MYCPE	Q8ewm7	mycoplasma
158	77	4.8	878	1	IL3E_MOUSE	P26954	mus musculu	231	74.5	4.6	255	1	RS2_LACLA	Q9cdr4	lactococcus
159	77	4.8	1643	1	RRPO_NMV	P15095	narcissus m	232	74.5	4.6	257	1	TARA_BACSU	Q8rki7	bacillus su
160	76.5	4.7	170	1	OBPB_HUMAN	Q9nph6	homo sapien	233	74.5	4.6	366	1	VE2_RHPV1	P22156	rhesus papi
161	76.5	4.7	342	1	TONB_PSEAE	Q51368	pseudomonas	234	74.5	4.6	468	1	6PGD_STAEP	Q8cp47	staphylococ
162	76.5	4.7	393	1	DEOB_THETN	Q8rcg6	thermoanaer	235	74.5	4.6	487	1	MMSA_BACSU	P42412	bacillus su
163	76.5	4.7	430	1	KDTA_CHLMU	Q9pk15	chlamydia m	236	74.5	4.6	492	1	ALG8_AZOVI	P94199	azotobacter
164	76.5	4.7	478	1	NIFD_METTL	P20620	methanococc	237	74.5	4.6	504	1	ARAG_ECOLI	P08531	escherichia
165	76.5	4.7	489	1	CPCU_RABIT	Q29510	oryctolagus	238	74.5	4.6	510	1	GPML_CLOAB	Q97153	clostridium
166	76.5	4.7	531	1	GPML_TRIHE	P59177	synecococc	239	74.5	4.6	513	1	LEU1_LACLA	Q02141	lactococcus
167	76.5	4.7	573	1	INAI_TRIHE	P34054	trichoderma	240	74.5	4.6	514	1	GPML_SALTY	Q8z156	salmonella
168	76.5	4.7	585	1	RHBC_RHIME	Q923r0	rhizobium m	241	74.5	4.6	693	1	IF2_CLOAB	Q97151	clostridium
169	76.5	4.7	710	1	ETF2_VACCA	O57220	vaccinia vi	242	74.5	4.6	710	1	ETF2_VARV	P33806	variola vir
170	76.5	4.7	710	1	ETF2_VACCC	P20635	vaccinia vi	243	74.5	4.6	715	1	ZF2_CANFA	P47983	canis famil
171	76.5	4.7	710	1	ETF2_VACCV	P20636	vaccinia vi	244	74.5	4.6	729	1	NTT7_BOVIN	Q9xs59	bos taurus
172	76.5	4.7	982	1	MSHM_SARGL	O63852	sarcophyton	245	74.5	4.6	987	1	YD94_METJA	Q58789	methanococc
173	76.5	4.7	1064	1	CARB_LACLA	Q9cfv2	lactococcus	246	74.5	4.6	1063	1	RBL1_MOUSE	Q64701	mus musculu
174	76.5	4.7	1274	1	MYPC_HUMAN	Q14896	homo sapien	247	74.5	4.6	1178	1	PH81_YEAST	P17442	saccharomyc
175	76.5	4.7	1616	1	RRPO_TOMS1	Q9ykd6	tomato mosa	248	74.5	4.6	3432	1	POLG_JAEV1	P27395	j genome po
176	76	4.7	322	1	NADA_AQUAE	O67730	aquifex aeo	249	74.5	4.6	3432	1	POLG_JAEV5	P19110	j genome po
177	76	4.7	345	1	YA03_TREPA	O83968	treponema p	250	74.5	4.6	329	1	CAHX_FLAPR	P32886	j genome po
178	76	4.7	376	1	MED7_SCHPO	O60104	schizosacch	251	74	4.6	380	1	APG2_ARCFU	P46281	flaveria pr
179	76	4.7	431	1	HISX_VIBVU	Q8d8q0	vibrio vuln	252	74	4.6				Q28847	archaeoglob

253	74	4.6	442	1	ENOA_LACPL	Q88yh3 lactobacill	326	72.5	4.5	663	1	RGPI_YEAST	P16664 saccharomyc
254	74	4.6	474	1	VP61_NPVOP	O10270 orgyia pseu	327	72.5	4.5	801	1	SYFB_STRPY	Q9a0i0 streptococc
255	74	4.6	502	1	P2BC_HUMAN	P48454 homo sapien	328	72.5	4.5	878	1	ACON_RICCN	Q92g90 rickettsia
256	74	4.6	504	1	MATK_ACTDE	Q95bz7 actinidia d	329	72.5	4.5	885	1	PODK_ENTHI	P372i3 entamoeba h
257	74	4.6	508	1	PD12_ATH	Q9srg3 arabidopsis	330	72.5	4.5	1091	1	DIA_DROME	P48608 drosophila
258	74	4.6	521	1	GPMI_METMA	Q9pyf8 methanosarc	331	72.5	4.5	1556	1	Y934_HUMAN	Q9y2e4 homo sapien
259	74	4.6	607	1	MM16_HUMAN	P51512 homo sapien	332	72.5	4.5	1616	1	RRPO_TOMK1	Q9glt8 tomato mosa
260	74	4.6	611	1	GLGB_FUSNN	Q8rf62 fusobacteri	333	72.5	4.5	1616	1	RRPO_TOMK2	P89676 tomato mosa
261	74	4.6	621	1	ILVB_MYCAV	Q59498 mycobacteri	334	72.5	4.5	1616	1	RRPO_TOML	P03587 tomato mosa
262	74	4.6	636	1	DNAK_PHOLL	Q7n8y4 photorhabdu	335	72.5	4.5	1675	1	CLH1_HUMAN	Q00610 homo sapien
263	74	4.6	638	1	DNAK_BUCAP	Q8k9y8 buchnera ap	336	72.5	4.5	1675	1	CLH_BOVIN	P49951 bos taurus
264	74	4.6	640	1	DNAK_VIBHA	O87384 vibrio harv	337	72.5	4.5	1675	1	CLH_RAT	P11442 rattus norv
265	74	4.6	709	1	SUL1_CAEEL	Q21376 caenorhabdi	338	72.5	4.5	2004	1	MYS3_HUMAN	Q92794 homo sapien
266	74	4.6	850	1	DPO1_ANATH	Q59156 anaerocellu	339	72.5	4.5	2222	1	DPOE_YEAST	P21951 saccharomyc
267	74	4.6	953	1	PODK_FLABI	Q39735 flaveria bi	340	72.5	4.5	2319	1	FA8_MOUSE	Q06194 mus musculu
268	74	4.6	960	1	FTSK_VIBCH	O84i33 vibrio chol	341	72.5	4.5	3175	1	RPOA_EAV	P19811 equine arte
269	74	4.6	1121	1	BMS1_SCHPO	Q94653 schizosacch	342	72.5	4.5	4367	1	DYHC_NEUCR	P45443 neurospora
270	74	4.6	1423	1	FRUA_STRMU	Q03174 streptococc	343	72	4.5	330	1	CAH1_FLALI	P46512 flaveria li
271	74	4.6	1447	1	BUD4_YEAST	P47136 saccharomyc	344	72	4.5	357	1	FULI_ACHFU	P35905 a fulicin p
272	74	4.6	4829	1	BIR6_HUMAN	Q9nr09 homo sapien	345	72	4.5	358	1	T2H2_HAEPA	P36433 haemophilus
273	73.5	4.5	146	1	HHB2_NAJNA	P22743 najja naja (	346	72	4.5	359	1	RS2_SPICI	P19679 spiroplasma
274	73.5	4.5	208	1	YCAC_ECOLI	P21367 escherichia	347	72	4.5	386	1	YA66_METJA	Q58466 methanococc
275	73.5	4.5	298	1	PNPP_SCHPO	Q00472 schizosacch	348	72	4.5	392	1	DEOB_STAAM	Q99x76 staphylococ
276	73.5	4.5	397	1	UXUA_YERPE	Q8zgz8 yersinia pe	349	72	4.5	395	1	DEOB_MYCPU	Q98gt4 mycoplasma
277	73.5	4.5	416	1	APMA_HUMAN	Q9hdc9 homo sapien	350	72	4.5	426	1	SCB1_MOUSE	Q9z2i9 mus musculu
278	73.5	4.5	447	1	G3PB_ATH	P25857 arabidopsis	351	72	4.5	461	1	GLMU_BUCAP	Q8ka74 buchnera ap
279	73.5	4.5	488	1	GATA_OCEIH	Q8es78 oceanobacil	352	72	4.5	464	1	LEU2_BACTN	Q8a617 bacteroides
280	73.5	4.5	505	1	GPMI_STAAM	Q99vk6 staphylococ	353	72	4.5	484	1	PEPD_ECOLI	P15288 escherichia
281	73.5	4.5	505	1	GPMI_STAAP	Q8nrl5 staphylococ	354	72	4.5	491	1	HSF1_CHICK	P38529 gallus gall
282	73.5	4.5	505	1	GPMI_STAEP	Q8cpx4 staphylococ	355	72	4.5	500	1	CPDK_MESAU	Q9qyg5 mesocricetu
283	73.5	4.5	514	1	GPMI_ECO57	Q8xde9 escherichia	356	72	4.5	510	1	GPMI_VIBVU	Q8dcw1 vibrio vuln
284	73.5	4.5	514	1	GPMI_ECOLI	P37689 escherichia	357	72	4.5	607	1	MM16_MOUSE	Q9wtr0 mus musculu
285	73.5	4.5	514	1	GPMI_SALTI	Q8z2f0 salmonella	358	72	4.5	607	1	MM16_RAT	O35548 rattus norv
286	73.5	4.5	514	1	GPMI_SHIFL	P59176 shigella fl	359	72	4.5	626	1	PPOC_LYCES	Q08305 lycopersico
287	73.5	4.5	542	1	EST6_DROMA	P47982 drosophila	360	72	4.5	630	1	PPOA_LYCES	Q08303 lycopersico
288	73.5	4.5	544	1	EST6_DROME	P08171 drosophila	361	72	4.5	634	1	GHR_BOVIN	P79108 bos taurus
289	73.5	4.5	710	1	ETF2_VACCT	Q9jfg3 vaccinia vi	362	72	4.5	656	1	DNLTJ_HELPY	O25336 helicobacte
290	73.5	4.5	1028	1	FTSK_VIBPA	Q87gp4 vibrio para	363	72	4.5	851	1	MUTS_STRPY	Q99xl8 streptococc
291	73.5	4.5	1044	1	RSG1_BOVIN	P09851 bos taurus	364	72	4.5	939	1	A2A2_HUMAN	O94973 h adapter-r
292	73.5	4.5	1071	1	CARB_NEIGO	Q59599 neisseria g	365	72	4.5	1036	1	YAN2_SCHPO	O10068 schizosacch
293	73.5	4.5	1111	1	SEC8_NEUCR	Q9he88 neurospora	366	72	4.5	1064	1	JMJ2_HUMAN	O75164 homo sapien
294	73.5	4.5	1944	1	ANC1_MOUSE	P33995 mus musculu	367	72	4.5	1129	1	YB95_YEAST	P38144 saccharomyc
295	73.5	4.5	2849	1	P1L1_HUMAN	Q8tdx9 homo sapien	368	72	4.5	1270	1	VGLN_CHICK	P81021 gallus gall
296	73.5	4.5	6684	1	R1AB_CVPPU	Q9iw06 p replicase	369	72	4.5	1443	1	DPO3_MYCPN	P75080 mycoplasma
297	73	4.5	470	1	VL2_HPV39	P24839 human papil	370	72	4.5	1502	1	N170_YEAST	P38181 saccharomyc
298	73	4.5	500	1	CPDR_MESAU	Q9qyg6 mesocricetu	371	72	4.5	1516	1	Y819_PSEAE	Q9hvt2 pseudomonas
299	73	4.5	525	1	Y912_METMA	Q8pyf0 methanosarc	372	72	4.5	2283	1	DPOE_MOUSE	Q9wvf7 mus musculu
300	73	4.5	533	1	GPMI_ANASP	Q8ypl2 anabaena sp	373	72	4.5	4344	1	DYHC_EMENI	P45444 emericella
301	73	4.5	564	1	FEP1_SCHPO	Q10134 schizosacch	374	71.5	4.4	241	1	NAGB_CLOAB	Q97mk9 clostridium
302	73	4.5	578	1	MDLB_BUCBP	Q89a96 buchnera ap	375	71.5	4.4	243	1	GCH1_YEAST	P51601 saccharomyc
303	73	4.5	618	1	ILVB_MYCTU	O53250 mycobacteri	376	71.5	4.4	261	1	YAC7_YEAST	P39735 saccharomyc
304	73	4.5	635	1	DNAK_VIBCH	Q34241 vibrio chol	377	71.5	4.4	273	1	Y133_METJA	Q57597 methanococc
305	73	4.5	649	1	DXS1_KITGR	Q9flv2 kitasatospo	378	71.5	4.4	317	1	KPRS_BRAJA	Q89dj1 bradyrhizob
306	73	4.5	738	1	ZN84_HUMAN	P51523 homo sapien	379	71.5	4.4	329	1	CCPA_STAXY	Q56194 staphylococ
307	73	4.5	1057	1	VP2_AHSV3	Q89508 african hor	380	71.5	4.4	343	1	RADA_HALVO	Q48328 halobacteri
308	73	4.5	1076	1	CARB_ARCFU	O28994 archaeoglob	381	71.5	4.4	394	1	DEOB_BACSU	P46353 bacillus su
309	73	4.5	1125	1	PHYA_POPTM	Q49934 populus tre	382	71.5	4.4	465	1	LEU2_BUCPS	P58945 buchnera ap
310	73	4.5	3063	1	CA1C_HUMAN	Q99715 homo sapien	383	71.5	4.4	484	1	PEN3_ADEP3	Q84176 porcine ade
311	73	4.5	4594	1	DYHC_HUMAN	Q14204 homo sapien	384	71.5	4.4	495	1	E1BL_ADE02	P03244 human adeno
312	73	4.5	4644	1	DYHC_RAT	P38650 rattus norv	385	71.5	4.4	515	1	GPMI_YERPE	Q8zjnn yersinia pe
313	72.5	4.5	223	1	YZL2_EBV	P03205 epstein-bar	386	71.5	4.4	519	1	SNX2_HUMAN	O60749 homo sapien
314	72.5	4.5	258	1	HIS6_KLEOX	P45603 klebsiella	387	71.5	4.4	562	1	MM25_HUMAN	Q9npa2 homo sapien
315	72.5	4.5	315	1	TRER_SALTY	P36674 salmonella	388	71.5	4.4	567	1	VE06_VARV	P33819 variola vir
316	72.5	4.5	385	1	OXDC_BACSU	O34714 bacillus su	389	71.5	4.4	600	1	IF2P_SULSO	Q980q8 sulfolobus
317	72.5	4.5	436	1	HISX_DEIRA	Q9rsi4 deinococcus	390	71.5	4.4	616	1	MUTA_STRCM	Q05064 streptomyce
318	72.5	4.5	505	1	GPMI_AGR75	Q8uaa5 agrobacteri	391	71.5	4.4	663	1	GR78_SCHPO	P36604 schizosacch
319	72.5	4.5	537	1	SYR_MYCPN	P75222 mycoplasma	392	71.5	4.4	816	1	SUS2_ORYSA	P31924 oryza sativ
320	72.5	4.5	555	1	ESTA_DROMI	O16168 drosophila	393	71.5	4.4	887	1	OBP_HSVB	P28947 equine herp
321	72.5	4.5	564	1	ASM1_CAEEL	Q10916 caenorhabdi	394	71.5	4.4	893	1	NIA_LEPMC	P36842 leptosphaer
322	72.5	4.5	575	1	MIS_BOVIN	P03972 bos taurus	395	71.5	4.4	899	1	POL_MMTVB	P03365 mouse mamma
323	72.5	4.5	606	1	MM17_HUMAN	Q9uiz9 homo sapien	396	71.5	4.4	985	1	AGLU_ASPOR	Q12558 aspergillus
324	72.5	4.5	617	1	FXK1_MOUSE	P42128 mus musculu	397	71.5	4.4	1006	1	BGAL_ASPNG	P29853 aspergillus
325	72.5	4.5	643	1	DNAK_CANBF	Q7vql4 candidatus	398	71.5	4.4	1014	1	FTK2_NEIMA	Q9juk9 neisseria m

399	71.5	4.4	1420	1	APX_XENLA	Q01613 xenopus lae	472	70	4.3	403	1	ALAF_CAVPO	P22324 cavia porce
400	71.5	4.4	1447	1	DCC_HUMAN	P43146 homo sapien	473	70	4.3	426	1	EXLP_TOBAC	Q03211 nicotiana t
401	71.5	4.4	2080	1	TOXC_COCCA	Q92215 c putative	474	70	4.3	436	1	THCB_RHOER	P43492 rhodococcus
402	71.5	4.4	3140	1	POLG_PPVRA	P17767 p genome po	475	70	4.3	442	1	HPPD_DAUCA	O23920 daucus caro
403	71.5	4.4	3141	1	POLG_PPVD	P13529 p genome po	476	70	4.3	451	1	RUN1_MOUSE	Q03347 m runt-rela
404	71.5	4.4	3830	1	SACS_MOUSE	Q9jlc8 mus musculu	477	70	4.3	451	1	YOD1_SCHPO	Q9uud8 schizosacch
405	71.5	4.4	4644	1	DYHC_MOUSE	Q9jhu4 mus musculu	478	70	4.3	465	1	SELA_DESBA	P56372 desulfovibr
406	71	4.4	286	1	PARB_CHLPN	Q9z7m0 chlamydia p	479	70	4.3	473	1	GCSB_HALN1	Q9hpk0 halobacteri
407	71	4.4	288	1	ACCD_PORPU	P51198 porphyra pu	480	70	4.3	480	1	DNAA_RHIME	P35890 rhizobium m
408	71	4.4	309	1	YQGH_BACSU	P46339 bacillus su	481	70	4.3	498	1	GALT_CLOPE	Q8xkp8 clostridium
409	71	4.4	325	1	HMGL_RAT	P97519 rattus norv	482	70	4.3	505	1	MATK_RHISY	Q9gfn8 rhizophora
410	71	4.4	327	1	PLSX_THEMEA	Q9wxz6 thermotoga	483	70	4.3	511	1	GPMT_STRCO	Q9l214 streptomyce
411	71	4.4	329	1	TRPB_ECO57	Q8x7b6 escherichia	484	70	4.3	532	1	GPMT_SYNY3	P74507 synechocyst
412	71	4.4	396	1	TRPB_ECOL6	Q8fhv9 escherichia	485	70	4.3	596	1	SYR_LEPIN	Q8f5j3 leptospira
413	71	4.4	396	1	TRPB_ECOLI	P00932 escherichia	486	70	4.3	611	1	PEPF_MYCPN	P54125 mycoplasma
414	71	4.4	407	1	DEOB_ECOLI	P07651 escherichia	487	70	4.3	637	1	DNAB_VIBPA	Q87rx3 vibrio para
415	71	4.4	412	1	AIAT_MUSCR	P26595 mus caroli	488	70	4.3	638	1	GHR_HUMAN	P10912 homo sapien
416	71	4.4	432	1	ENO_ENTHR	Q8gr70 enterococcu	489	70	4.3	673	1	UVRB_BORBU	O51776 borrelia bu
417	71	4.4	437	1	ORPI_MOUSE	Q91x19 mus musculu	490	70	4.3	786	1	FL10_CHLRE	P46869 chlamydomon
418	71	4.4	473	1	SYC_METWA	Q8pvc1 methanosarc	491	70	4.3	801	1	FTSK_STRPY	Q9a155 streptococc
419	71	4.4	509	1	NRM3_ARATH	Q9snv9 arabidopsis	492	70	4.3	851	1	MUTS_STRP3	Q8k5j5 streptococc
420	71	4.4	510	1	GPMT_VIBCH	Q9kv22 vibrio chol	493	70	4.3	921	1	RB_MOUSE	P13405 mus musculu
421	71	4.4	568	1	GGT1_RAT	P07314 rattus norv	494	70	4.3	943	1	SYI_PSEFL	P18330 pseudomonas
422	71	4.4	579	1	COE2_BRARE	Q93375 brachydanio	495	70	4.3	949	1	PODK_MESCR	Q42910 mesembryant
423	71	4.4	585	1	SYR_AGR15	Q8uep4 agrobacteri	496	70	4.3	994	1	DPO2_KLUJA	P05468 kluyveromyc
424	71	4.4	585	1	TFH1_DROME	Q960e8 drosophila	497	70	4.3	1026	1	TAC2_HUMAN	O95359 homo sapien
425	71	4.4	621	1	APS_MOUSE	Q9jid9 mus musculu	498	70	4.3	2116	1	MYS2_DICDI	P08799 dictyosteli
426	71	4.4	682	1	RECG_BACSU	O34942 bacillus su	499	70	4.3	2174	1	T240_HUMAN	Q9uhv7 homo sapien
427	71	4.4	777	1	LON_BUCAI	P57549 buchnera ap	500	70	4.3	2748	1	NUM1_YEAST	Q00402 saccharomyc
428	71	4.4	875	1	SYL_RHILO	Q98eu7 rhizobium l							
429	71	4.4	1027	1	ISW1_DROME	Q24368 drosophila							
430	71	4.4	1132	1	BAT3_HUMAN	P46379 homo sapien							
431	71	4.4	1197	1	EVGS_ECOLI	P30855 escherichia							
432	71	4.4	1401	1	LATA_LATWA	P23631 latrodectus							
433	71	4.4	4639	1	DYHC_DROME	P37276 drosophila							
434	70.5	4.4	146	1	HBB_MESAU	P02094 mesocricetu							
435	70.5	4.4	178	1	YE71_METJA	Q58866 methanococc							
436	70.5	4.4	333	1	GIPC_RAT	Q92254 rattus norv							
437	70.5	4.4	343	1	E2B_THEMEA	Q9x013 thermotoga							
438	70.5	4.4	352	1	TX37_CABEL	Q9u2c9 caenorhabdi							
439	70.5	4.4	353	1	TPO_HUMAN	P40225 homo sapien							
440	70.5	4.4	378	1	KLP2_BONMO	P46874 bombyx mori							
441	70.5	4.4	388	1	DEOB_DEIRA	Q9rs19 deinococcus							
442	70.5	4.4	393	1	DEOB_BACST	O24821 bacillus st							
443	70.5	4.4	401	1	CGB1_ORYJA	Q9dga0 oryzias jav							
444	70.5	4.4	441	1	GDF9_MOUSE	Q07105 mus musculu							
445	70.5	4.4	449	1	NYR_DROME	P25931 drosophila							
446	70.5	4.4	494	1	VPE_CITSI	P49043 citrus sine							
447	70.5	4.4	508	1	C6D5_DROME	Q9vfp1 drosophila							
448	70.5	4.4	514	1	T3RH_HAEIN	P44105 haemophilus							
449	70.5	4.4	527	1	MM19_MOUSE	Q9jhi0 mus musculu							
450	70.5	4.4	529	1	HSF1_HUMAN	Q00613 homo sapien							
451	70.5	4.4	531	1	YTGF_LACLA	Q9cee2 lactococcus							
452	70.5	4.4	585	1	ESR1_ORENI	Q02092 gallicus gall							
453	70.5	4.4	608	1	GHR_CHICK	Q9epz6 mus musculu							
454	70.5	4.4	613	1	TX18_MOUSE	Q15256 homo sapien							
455	70.5	4.4	657	1	PTPR_HUMAN	O12525 methanobact							
456	70.5	4.4	658	1	VATI_METTH	O27041 methanobact							
457	70.5	4.4	805	1	TERA_XENLA	P23787 xenopus lae							
458	70.5	4.4	914	1	SYA_PYRFU	Q8u425 pyrococcus							
459	70.5	4.4	961	1	ACON_MYCAV	O08451 mycobacteri							
460	70.5	4.4	1382	1	INSR_HUMAN	P06213 homo sapien							
461	70.5	4.4	1625	1	CTPI_MYCTU	Q10900 mycobacteri							
462	70.5	4.4	2738	1	PGCV_RAT	Q9erb4 rattus norv							
463	70.5	4.4	4377	1	ANK3_HUMAN	Q12955 homo sapien							
464	70	4.3	187	1	RL5_MYCTU	P95064 mycobacteri							
465	70	4.3	236	1	Y141_METTH	O26244 methanobact							
466	70	4.3	249	1	YF82_METJA	Q58977 methanococc							
467	70	4.3	260	1	ARGT_SALTY	P02911 salmonella							
468	70	4.3	364	1	PLCE_HUMAN	Q9nuq2 homo sapien							
469	70	4.3	386	1	SUCC_DEIRA	Q9ruy3 deinococcus							
470	70	4.3	390	1	TGF1_HORSE	O19011 equus cabal							
471	70	4.3	397	1	APGM_METWA	Q8px04 methanosarc							

ALIGNMENTS

RESULT 1

ID	YA93_SCHPO	STANDARD	PRT	758 AA.
AC	Q09782;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Hypothetical protein C13G6.03 in chromosome 1.			
GN	SPAC13G6.03.			
OS	Schizosaccharomyces pombe (Fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;			
OC	Schizosaccharomycetes.			
OX	NCBI_TaxID=4896;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RX	MEDLINE=21848401; PubMed=11859360;			
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,			
RA	Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,			
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,			
RA	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,			
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,			
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,			
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,			
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,			
RA	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,			
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,			
RA	Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,			
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,			
RA	Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,			
RA	Wetjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,			
RA	Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,			
RA	Borzum K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,			
RA	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,			
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,			
RA	Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,			
RA	Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,			
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,			





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RESULT 3
PIGO MOUSE
ID PIGO MOUSE STANDARD; PRT; 1093 AA.
AC Q9JJ16; Q9CRY2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-glycan biosynthesis, class O protein (PIG-O).
GN PIGO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RC TISSUE=Testis;
RX MEDLINE=20347191; PubMed=10781593;
RA Hong Y., Maeda Y., Watanabe R., Inoue N., Ohishi K., Kinoshita T.;
RT "Requirement of PIG-F and PIG-O for transferring phosphoethanolamine to
RT the third mannose in glycosylphosphatidylinositol.";
RL J. Biol. Chem. 275:20911-20919(2000).
RN [2]
RP SEQUENCE OF 931-1101 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuka S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Involved in GPI-anchor biosynthesis but not essential
CC for this process. Involved, together with PIGF, in the transfer of
CC ethanolamine phosphate to the third mannose of GPI.
CC -!- PATHWAY: GPI-anchor biosynthesis.
CC -!- SUBUNIT: Forms a complex with PIGF. PIGF is required to stabilize
CC PIGO.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum.
CC
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CC or send an email to license@isb-sib.ch).
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FT TRANSMEM 512 532 POTENTIAL.
FT TRANSMEM 669 689 POTENTIAL.
FT TRANSMEM 702 722 POTENTIAL.
FT TRANSMEM 748 768 POTENTIAL.
FT TRANSMEM 831 851 POTENTIAL.
FT TRANSMEM 856 876 POTENTIAL.
FT TRANSMEM 945 965 POTENTIAL.
FT TRANSMEM 1018 1038 POTENTIAL.
FT TRANSMEM 1052 1072 POTENTIAL.
FT CONFLICT 1000 1000 V -> M (IN REF. 2).
SQ SEQUENCE 1093 AA; 119156 MW; AB641F9F3527296C CRC64;

Query Match 30.3%; Score 490; DB 1; Length 1093;
Best Local Similarity 40.5%; Pred. No. 2.1e-33;
Matches 118; Conservative 41; Mismatches 108; Indels 24; Gaps 7;

QY 19 GIAVFLRGFPFAPVRSSARAHEGAEAP-PAPEPSAGASSNWTTLPPPLFSKVIVLIDALR 77
Db 20 GIALFTSGFLLRLRLTNQSSCQELPGPGPLPWGSHGKPGACWMPSPRSFRRVVLVLDALR 79
QY 78 DDF-----VFGSKGVKFMPTTYL-----VEKGASHS--FVAEAKPPTVTMPRIKAL 122
Db 80 DFEAQPORSHVPGEPVS-VPLFGKLGSLQRILESQPHGRLYRSQVDPPTTQRLKAL 138
QY 123 MTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIYFVGDETVVKLFPHKHFVEYDGTTS 182
Db 139 TTGSLPTFIDAGSNFASHAIVEDNVIQQLNSAGRRRVVFMGDDTWRDLFPGAFSAFFFS 198
QY 183 FFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDIGHISGPNPLGQKLSMDSV 242
Db 199 FNVRLDHTVDNGILEHLYPTLDGSDVDLIAHFLGVHDGKHGPHPEMAKLSQMDQV 258
QY 243 LMKIHTSLQSKERETPLPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILIS 293
Db 259 IQGL---IERLENDT---LLVVAGDHGTMNGDHGSDSELEVSALFLYS 302

RESULT 4
PIGO HUMAN
ID PIGO HUMAN STANDARD; PRT; 1088 AA.
AC Q8TEQ8; Q8TDS8; Q96CS9; Q9BVN9; Q9Y4B0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phosphatidylinositol-glycan biosynthesis, class O protein (PIG-O).
GN PIGO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RA Ansorge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Ganes J., Danganan L., Poundstone P.,
RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
RA Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
RA Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RT "Sequence analysis of a human P1 clone containing the XRCC9 DNA repair
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:24:48 ; Search time 53 Seconds  
(without alignments)  
1652.636 Million cell updates/sec

Title: US-10-036-150-45  
Perfect score: 1617  
Sequence: 1 MRLSGTFATCCVAIEVLGI.....LISSAFERKPGDIRHPKHVQ 310

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB ID	Description
		Match	Length		
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2	1617	100.0	310	4 AAY72877	Aay72877 Human PRO
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4	1617	100.0	310	5 AAU83650	Aau83650 Human PRO
5	1617	100.0	310	5 ABG95920	Abg95920 Human sec
6	1617	100.0	310	5 ABB84962	Abb84962 Human PRO
7	1617	100.0	310	5 ABB95568	Abb95568 Human ang
8	1617	100.0	310	6 ABU69112	Abu69112 Human PRO
9	1617	100.0	310	6 ABU80797	Abu80797 Human PRO
10	1617	100.0	310	6 ABO33763	Aboc33763 Novel hum
11	1617	100.0	310	6 ABU90945	Abu90945 Novel hum
12	1617	100.0	310	6 ABO34004	Aboc34004 Human sec
13	1617	100.0	310	6 ABO19428	Aboc19428 Human sec
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16	1617	100.0	310	6 ABU72356	Abu72356 Human PRO
17	1617	100.0	310	6 ABG74761	Abg74761 Human PRO
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96	1617	100.0	310	8 ADE41542	Ade41542 Human sec
97	1617	100.0	310	8 ADE21238	Ade21238 Novel hum
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102	1617	100.0	310	8	ADD74327	Human PRO	175	481	29.7	1089	6	ABR66879	Human sec
103	1617	100.0	310	8	ADD76057	Novel hum	176	481	29.7	1089	6	ABO16092	Human sec
104	1617	100.0	310	8	ADD85549	Novel hum	177	481	29.7	1089	6	ABO13798	Human sec
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119	1617	100.0	975	4	AAM933346	Human pol	192	481	29.7	1089	6	ABR60168	Human sec
120	1610	99.6	983	7	ADE07999	Novel pro	193	481	29.7	1089	6	ABR67903	Human sec
121	1609	99.5	310	7	ADB85713	Novel hum	194	481	29.7	1089	6	ABR65291	Human sec
122	1601	99.0	310	6	ABO34236	Human sec	195	481	29.7	1089	6	ABR68513	Human sec
123	1194	73.8	236	4	AAB50931	Human PRO	196	481	29.7	1089	6	ABR71925	Human sec
124	1156	71.5	894	4	AAM93761	Human pol	197	481	29.7	1089	6	ABU85405	Human PRO
125	922	57.0	271	7	ADE09044	Novel pro	198	481	29.7	1089	6	ABU89095	Human sec
126	511.5	31.6	880	4	ABB58897	Drosophil	199	481	29.7	1089	6	ABU83175	Human sec
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131	481	29.7	896	4	AAM24250	Human EST	204	481	29.7	1089	6	ABR64986	Human sec
132	481	29.7	1089	3	AAV99369	Human PRO	205	481	29.7	1089	6	ABR68818	Human sec
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295	481	29.7	1089	6	ABO36229	Abo36229 Human PRO	368	481	29.7	1089	6	ABM22113	Abm22113 Human sec
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297	481	29.7	1089	6	ABM76458	Abm76458 Human sec	370	481	29.7	1089	6	ABM28518	Abm28518 Human sec
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583	481	29.7	1089	7	ABO06939	Human sec
584	481	29.7	1089	7	ABR84892	Human sec
585	4					













CC solid support. The proteins are useful for linking a bioactive molecule  
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,  
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.  
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,  
CC or I, or antibodies against them are useful for modulating a biological  
CC activity of a cell expressing a polypeptide designated as A, B, C or D or  
CC E, F, G, H, or I. The cell is killed. The proteins are useful for  
CC identifying agonists or antagonists, for the preparation of a medicament  
CC useful in the treatment of a condition which is responsive to the  
CC proteins, as molecular weight markers for protein electrophoresis  
CC purposes, and as therapeutic agents for treating sports-related joint  
CC problems, articular cartilage defects, osteoarthritis or rheumatoid  
CC arthritis. Nucleic acids encoding the proteins are useful as  
CC hybridisation probes, in chromosome and gene mapping, in the generation  
CC of anti-sense RNA and DNA, for the preparation of the proteins, to  
CC generate transgenic or knockout animals which are useful in the  
CC development and screening of therapeutic useful reagents, for chromosome  
CC identification, and in gene therapy. The antibody is useful as a  
CC therapeutic agent, in a diagnostic assay and for affinity purification of  
CC the protein from recombinant cell culture natural sources. The present  
CC sequence represents a novel secreted or transmembrane protein of the  
CC invention

XX Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 5; Length 310;  
Best Local Similarity 100.0%; Pred. No. 4.6e-159;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRLSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHAEPPAPEPSAGASSNWTTL 60  
QY 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIK 120  
Db 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIK 120  
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAAGKRIVFYGDETWVKLFPKHFEVDGT 180  
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAAGKRIVFYGDETWVKLFPKHFEVDGT 180  
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIGHISGNSPLIGQKLEMD 240  
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIGHISGNSPLIGQKLEMD 240  
QY 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
QY 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 6  
ABB84962  
ID ABB84962 standard; protein; 310 AA.  
XX  
AC ABB84962;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Human PRO4405 protein sequence SEQ ID NO:292.  
XX

KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX wound healing; chromosome mapping; gene mapping.

OS Homo sapiens.  
XX WO200200690-A2.  
XX 03-JAN-2002.  
XX 20-JUN-2001; 2001WO-US019692.  
XX 23-JUN-2000; 2000US-0213637P.  
PR 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220664P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 02-AUG-2000; 2000US-0222695P.  
PR 17-AUG-2000; 2000US-00643657.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 24-OCT-2000; 2000US-0242922P.  
PR 08-NOV-2000; 2000US-00709238.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.

(GETH ) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-090516/12.  
N-PSDB; ABL88217.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
infarction), endothelial or angiogenic disorders in a mammal.

Claim 11; Fig 292; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
antiangiogenic, hypotensive, vulnery and antiarteriosclerotic  
activities, and can be used in gene therapy. The PRO polynucleotides,  
proteins, agonists and antagonists are useful for treating or diagnosing  
a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
healing. The PRO polynucleotides have applications in molecular biology,  
including use as hybridisation probes, and in chromosome and gene  
mapping. ABL88259 to ABL88267 represent primers and probes used in the  
exemplification of the present invention

```
XX SQ Sequence 310 AA;
Query Match 100.0%; Score 1617; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60
Db 1 MRLSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60

QY 61 PPPLFSKVIVLIDALRDDVFVSGKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDVFVSGKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120

QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDFTWVKLFPHFVEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDFTWVKLFPHFVEYDGT 180

QY 181 TSFFVSDYTEVDNNTVTRHLDKVLKRGDWDILILHYLGLDHIHISGPNPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNTVTRHLDKVLKRGDWDILILHYLGLDHIHISGPNPLIGQKLSMD 240

QY 241 SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300

QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310
```

```
RESULT 7
ABB95568
ID ABB95568 standard; protein; 310 AA.
AC ABB95568;
XX 19-JUL-2002 (first entry)
DT Human angiogenesis related protein PRO4405 SEQ ID NO: 292.
DE
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cystostatic; antiangiogenic; hypotensive; vulnery;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX WO200208284-A2.
XX 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
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PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-171999/22.
DR N-PSDB; ABL95706.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 292; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
SQ Sequence 310 AA;
Query Match 100.0%; Score 1617; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60
Db 1 MRLSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60

QY 61 PPPLFSKVIVLIDALRDDVFVSGKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDVFVSGKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120

QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDFTWVKLFPHFVEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDFTWVKLFPHFVEYDGT 180
```

Db	121	ALMTGSLPGFVDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHVEYDGT	180
Qy	181	TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHGHISGPNSPILICQKLSEMD	240
Db	181	TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHGHISGPNSPILICQKLSEMD	240
Qy	241	SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP	300
Db	241	SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP	300
Qy	301	GDIRHPKHVQ 310	
Db	301	GDIRHPKHVQ 310	

RESULT 8  
ABU69112  
ID ABU69112 standard; protein; 310 AA.

PR	22-MAY-2000;	2000WO-US014042.
PR	02-JUN-2000;	2000WO-US015264.
PR	23-AUG-2000;	2000WO-US023522.
PR	24-AUG-2000;	2000WO-US023328.
PR	01-DEC-2000;	2000WO-US032678.
PR	20-DEC-2000;	2000WO-US034956.
PR	28-FEB-2001;	2001WO-US006520.
PR	01-JUN-2001;	2001WO-US017800.
PR	20-JUN-2001;	2001WO-US019692.
PR	29-JUN-2001;	2001WO-US021066.
PR	09-JUL-2001;	2001WO-US021735.
PR	16-AUG-2001;	2001US-00931836.
XX	(GETH ) GENENTECH INC.	
PA		
XX		
PI	Desnoyers L,	Eaton DL,
PI	Stewart TA,	Watanabe CK,
XX		
DR	WPI ;	2003-341962/32.
DR	N-PSDB; ACA05159.	

Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889, PRO1890, PRO1897, PRO1785, PRO4353, useful for treating sports injuries, arthritis, diabetes, obesity, hyper- or hypo-insulinemia.

Claim 12; Fig 20; 194pp; English.

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful in diagnosing or treating various bone and/or cartilage disorders (e.g. sports injuries, arthritis), various insulin deficient states (e.g. diabetes mellitus, hypo-insulinaemia), obesity, hyper-insulinaemia, haemoglobin-associated disorders (e.g. thalassaemias), kidney disorders associated with decreased mesangial cell function (e.g. Berger disease), or other nephropathies associated with Schonlein-Henoch purpura, celiac disease, dermatitis herpetiformis or Crohn's disease. The PRO polynucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. They are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals on knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. Anti-PRO antibodies may be used in diagnostic assays for PRO polypeptides, or for the affinity purification of the polypeptides from recombinant cell culture or natural sources. ABU69103-ABU69125 represent the human PRO polypeptides of the invention



QY	241	SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP	300
Db	241	SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP	300
QY	301	GDIRHPKHVQ	310
Db	301	GDIRHPKHVQ	310
RESULT 9			
ABU80797			
ID	ABU80797	standard; protein; 310 AA.	
XX			
AC	ABU80797;		
DT			
XX	23-JUN-2003	(first entry)	
XX			
DE	Human PRO polypeptide #59.		
XX			
KW	Human; PRO polypeptide; secreted and transmembrane protein;		
KW	anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.		
XX			
OS	Homo sapiens;		
XX			
PN	US2003036635-A1.		
XX			
PD	20-FEB-2003.		
XX			
PF	28-AUG-2002; 2002US-00230163.		
XX			
PR	25-JUL-2000; 2000US-0220638P;		
PR	01-JUN-2001; 2001WO-US017800.		
PR	29-JUN-2001; 2001WO-US021066.		
PR	09-APR-2002; 2002US-00119480.		
XX			
PA	(GETH ) GENENTECH INC.		
XX			
PI	Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;		
PI	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;		
XX			
DR	WPI; 2003-342045/32.		
DR	N-PSDB; ACA66899.		
XX			
PT	One hundred and twenty two nucleic acids encoding PRO polypeptides;		
PT	useful for the manufacture of a medicament for diagnosing or treating		
PT	tumor.		
XX			
PS	Claim 11; Fig 118; 314pp; English.		
XX			
CC	The present invention relates to the isolation of novel human PRO		
CC	polypeptides, and the polynucleotide sequences encoding them. The PRO		
CC	polypeptides are secreted and transmembrane proteins. The PRO		
CC	polypeptides and polynucleotides are useful for preparing a medicament		
CC	useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are		
CC	useful in diagnostic assays for PRO, by detecting its expression in		
CC	specific cells, tissues or serum, and for affinity purification of PRO		
CC	from recombinant cell culture or natural sources. ABU80739-ABU80860		
CC	represent the human PRO polypeptides of the invention. Note: The sequence		
CC	data for this patent was obtained in electronic format directly from the		
CC	USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html		
XX			
SQ	Sequence 310 AA;		
Query Match 100.0%; Score 1617; DB 6; Length 310;			
Best Local Similarity 100.0%; Pred. No. 4.6e-159;			
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
QY	1	MRLSGGTATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPFPAPEPSAGASSNWTTL	60
Db	1	MRLSGGTATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPFPAPEPSAGASSNWTTL	60
QY	61	PPPLFSKVIVLIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK	120



09-JAN-2003 .

01-MAY-2002; 2002US-00063519.

30-DEC-1998; 98KR-00062142.

08-MAR-1999; 99WO-US005028.

14-MAY-1999; 99US-00311832.

14-MAY-1999; 99WO-US010733.

25-AUG-1999; 99US-00380137.

25-AUG-1999; 99US-00380138.

25-AUG-1999; 99US-00380139.

25-AUG-1999; 99US-00380142.

15-SEP-1999; 99US-00397342.

18-OCT-1999; 99US-00403297.

12-NOV-1999; 99US-00423844.

30-DEC-1999; 99WO-US031274.

18-FEB-2000; 2000WO-US004341.

01-MAR-2000; 2000WO-US005601.

02-MAR-2000; 2000WO-US005841.

21-MAR-2000; 2000WO-US007532.

22-MAY-2000; 2000WO-US014042.

02-JUN-2000; 2000WO-US015264.

22-AUG-2000; 2000US-00644848.

24-AUG-2000; 2000WO-US023328.

18-SEP-2000; 2000US-00664610.

18-SEP-2000; 2000US-00665350.

08-NOV-2000; 2000US-00709238.

10-NOV-2000; 2000WO-US030873.

01-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000US-00747259.

20-DEC-2000; 2000WO-US034956.

28-FEB-2001; 2001WO-US006520.

22-MAR-2001; 2001US-00816744.

10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854280.

30-MAY-2001; 2001US-00870574.

01-JUN-2001; 2001WO-US017800.

05-JUN-2001; 2001US-00874503.

29-JUN-2001; 2001US-00869599.

18-JUL-2001; 2001US-00908827.

06-DEC-2001; 2001US-00006867.

(GETH ) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
WFI; 2003-447384/42.  
N-PSDB; ACD81610.

New isolated antibody specifically binding a PRO polypeptide, useful for the preparation of a medicament for treating disorders with the aberrant expression or activity of the PRO polypeptide, such as tumor conditions and cancer.

Disclosure; Fig 140; 223pp; English.

The invention relates to an antibody that binds to a secreted or transmembrane protein designated PRO1446 appearing as ABO33941. The protein is one of 84 PRO polypeptides which (along with their encoding nucleic acids) are disclosed in the specification. The methods and compositions of the present invention are useful for the preparation of a medicament for the treatment of disorders associated with the aberrant expression or activity of the PRO polypeptide, such as tumour conditions and cancer. They can also be used to generate transgenic or knockout animals useful in the development and screening of therapeutically useful reagents. The PRO polypeptides and encoding nucleic acids can be used as molecular weight markers for protein electrophoresis, chromosome identification and tissue typing. The antibodies may be used in various diagnostic, competitive binding and/or immunoprecipitation assays. The present sequence represents a PRO polypeptide

Sequence 310 AA;



PR 14-MAY-1999; 99WO-US010733.  
PR 25-MAY-1999; 99US-0135750P.  
PR 08-JUN-1999; 99US-0138166P.  
PR 20-JUL-1999; 99US-0144791P.  
PR 03-AUG-1999; 99US-0146970P.  
PR 25-AUG-1999; 99US-00380142.  
PR 29-OCT-1999; 99US-0162506P.  
PR 02-DEC-1999; 99WO-US028551.  
PR 22-DEC-1999; 99WO-US030720.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 22-AUG-2000; 2000US-00644848.  
PR 23-AUG-2000; 2000WO-US023328.  
PR 24-AUG-2000; 2000WO-US032678.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001US-00869599.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
PI  
XX  
DR WPI; 2003-492030/46.  
DR N-PSDB; ACD28828.  
XX  
XX New isolated, secreted and transmembrane PRO polypeptides and encoding  
PT nucleic acids, useful for the diagnosis and treatment of disorders such  
PT as diabetes, obesity and/or hypoinsulinemia.  
XX  
XX Claim 12; Fig 20; 196pp; English.  
PS  
XX The invention relates to a new isolated nucleic acid which encodes a PRO  
CC polypeptide. The methods and compositions of the present invention are  
CC useful for the diagnosis and treatment of disorders associated with the  
CC PRO polypeptides, such as diabetes, obesity and hypoinsulinaemia. The  
CC present sequence represents the amino acid sequence of a human secreted  
CC and transmembrane PRO polypeptide  
XX  
XX Sequence 310 AA;  
Query Match 100.0%; Score 1617; DB 6; Length 310;  
Best Local Similarity 100.0%; Pred. No. 4.6e-159;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60  
Db |||||||  
QY 61 PPPLFSKVIVLIDALRDDDFVFGSGKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIK 120  
Db |||||||  
QY 61 PPPLFSKVIVLIDALRDDDFVFGSGKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIK 120  
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDSDVIRQAKAGKRIVFYGDETWVKLFPPKHFEYDGT 180  
Db |||||||  
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDSDVIRQAKAGKRIVFYGDETWVKLFPPKHFEYDGT 180  
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGNSPLIGQKLSEMD 240  
Db |||||||  
181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGNSPLIGQKLSEMD 240

QY 241 SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db |||||||  
241 SVLMKIHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
QY 301 GDIRHPKHVQ 310  
Db |||||||  
301 GDIRHPKHVQ 310  
RESULT 14  
ABU72021  
ID ABU72021 standard; protein; 310 AA.  
XX  
AC ABU72021;  
XX  
DT 11-JUN-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO4405.  
XX  
KW Human; secreted and transmembrane polypeptide; chromosome mapping;  
KW gene mapping; transgenic animal; knockout animal;  
KW therapeutic agent screening; chromosome identification; tissue typing;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2003018183-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 01-MAY-2002; 2002US-00063512.  
XX  
PR 06-DEC-2001; 2001US-00006867.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX  
XX WPI; 2003-330984/31.  
DR N-PSDB; ACA60432.  
XX  
XX New secreted and transmembrane PRO polypeptides and nucleic acid  
PT molecules encoding the polypeptides, useful in gene therapy or preparing  
PT a medicament for treating a condition that is responsive to the PRO  
PT polypeptide or antibody.  
PS Disclosure; Fig 140; 409pp; English.  
XX  
CC The invention describes novel isolated PRO polypeptides. The PRO  
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament  
CC for treating a condition that is responsive to the PRO polypeptide or  
CC antibody. The PRO nucleotide sequences may be used as hybridisation  
CC probes in chromosome and gene mapping, or in generating antisense RNA and  
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knockout animals, which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides and nucleic acid molecules are also useful in gene  
CC therapy, and as molecular weight markers for protein electrophoresis  
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for  
CC PRO, or for the affinity purification of PRO from recombinant cell  
CC culture or natural sources. This is the amino acid sequence of a novel  
CC human secreted and transmembrane PRO polypeptide  
XX  
SQ Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 6; Length 310;  
Best Local Similarity 100.0%; Pred. No. 4.6e-159;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFATCCVAIEVLGIAVFLRGFFFPAPVRSSARAETHGAEPPEPSAGASSNWTTL 60  
Db 1 MRLGSGTFATCCVAIEVLGIAVFLRGFFFPAPVRSSARAETHGAEPPEPSAGASSNWTTL 60  
QY 61 PPPLFSKVIVILDALRDDVFVSGKGVKMPYTTTLYLVEKGASHSFVAEAKPPTVTPRIK 120  
Db 61 PPPLFSKVIVILDALRDDVFVSGKGVKMPYTTTLYLVEKGASHSFVAEAKPPTVTPRIK 120  
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDSDVIRQAKAAGKRVFYGDETWVKLFPKHVEYDGT 180  
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDSDVIRQAKAAGKRVFYGDETWVKLFPKHVEYDGT 180  
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHLYGLDGHIGHISGPNPLIGQKLSMD 240  
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHLYGLDGHIGHISGPNPLIGQKLSMD 240  
QY 241 SVLMKIHTSLQSKERETPLPDLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db 241 SVLMKIHTSLQSKERETPLPDLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
QY 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 15  
ABU71575  
ID ABU71575 standard; protein; 310 AA.  
XX  
AC ABU71575;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Human secreted polypeptide PRO4405.  
XX  
KW Human; gene therapy; tumour; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US2003013855-A1.  
XX  
PD 16-JAN-2003.  
XX  
PF 03-MAY-2002; 2002US-00063616.

XX 30-DEC-1998; 98KR-00062142.  
PR 08-MAR-1999; 99WO-US005028.  
PR 14-MAY-1999; 99US-00311832.  
PR 14-MAY-1999; 99WO-US010733.  
PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.  
PR 25-AUG-1999; 99US-00380139.  
PR 25-AUG-1999; 99US-00380142.  
PR 15-SEP-1999; 99US-00397342.  
PR 18-OCT-1999; 99US-00403297.  
PR 12-NOV-1999; 99US-00423844.  
PR 30-DEC-1999; 99WO-US031274.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 08-NOV-2000; 2000US-00709238.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
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PR 29-JUN-2001; 2001US-00869599.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-DEC-2001; 2001US-00006867.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX  
DR WPI; 2003-330485/31.  
DR N-PSDB; ACA58879.  
XX  
PT New isolated antibody specifically binding a PRO polypeptide, useful for  
PT the preparation of a medicament for treating disorders with the aberrant  
PT expression or activity of the PRO polypeptide, such as tumor conditions  
PT and cancer.  
XX  
PS Example 16; Page 212-213; 406pp; English.  
XX

CC The invention relates to an antibody that binds to a polypeptide with a  
CC fully defined sequence given in the specification. The methods and  
CC compositions (containing antibodies that specifically bind a PRO  
CC polypeptide) of the present invention are useful for the preparation of a  
CC medicament for the treatment of disorders associated with the aberrant  
CC expression or activity of the PRO polypeptide, such as tumour conditions  
CC and cancer. They can also be used to generate transgenic or knockout  
CC animals useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as  
CC molecular weight markers for protein electrophoresis, chromosome  
CC identification and tissue typing. The PRO polypeptides are useful to  
CC induce angiogenesis e.g wound healing; in the treatment of sports-related  
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid  
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The  
CC antibodies may be used in various diagnostic, competitive binding and/or  
CC immunoprecipitation assays. The present sequence represents the amino  
CC acid sequence of a PRO polypeptide of the invention  
XX  
SQ Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 6; Length 310;  
Best Local Similarity 100.0%; Pred. No. 4.6e-159;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:28:44 ; Search time 46 Seconds  
(without alignments)  
2113.950 Million cell updates/sec

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Perfect score: 1617  
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Post-processing: Minimum Match 0%  
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	1617	100.0	310	12	US-10-219-535-118	Sequence 118, App
4	1617	100.0	310	12	US-10-232-230-118	Sequence 118, App
5	1617	100.0	310	12	US-10-063-745-140	Sequence 140, App
6	1617	100.0	310	12	US-10-063-512-140	Sequence 140, App
7	1617	100.0	310	12	US-10-063-513-140	Sequence 140, App
8	1617	100.0	310	12	US-10-063-515-140	Sequence 140, App
9	1617	100.0	310	12	US-10-063-549-140	Sequence 140, App
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238	1617	100.0	310	14	US-10-063-684-140	Sequence 140, App	311	481	29.7	1089	12	US-10-198-758-266	Sequence 266, App
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242	1617	100.0	310	14	US-10-063-647-140	Sequence 140, App	315	481	29.7	1089	12	US-10-199-313-266	Sequence 266, App
243	1617	100.0	310	14	US-10-218-765-118	Sequence 118, App	316	481	29.7	1089	12	US-10-199-456-266	Sequence 266, App
244	1617	100.0	310	14	US-10-219-063-118	Sequence 118, App	317	481	29.7	1089	12	US-10-201-329-266	Sequence 266, App
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405	481	29.7	1089	14	US-10-180-541-266	Sequence 266, App	478	481	29.7	1089	14	US-10-196-762-266	Sequence 266, App
406	481	29.7	1089	14	US-10-187-886-266	Sequence 266, App	479	481	29.7	1089	14	US-10-197-695-266	Sequence 266, App
407	481	29.7	1089	14	US-10-187-886-266	Sequence 266, App	480	481	29.7	1089	14	US-10-195-894-266	Sequence 266, App
408	481	29.7	1089	14	US-10-180-548-266	Sequence 266, App	481	481	29.7	1089	14	US-10-006-856A-102	Sequence 266, App
409	481	29.7	1089	14	US-10-180-551-266	Sequence 266, App	482	481	29.7	1089	14	US-10-176-484-266	Sequence 266, App
410	481	29.7	1089	14	US-10-180-998-266	Sequence 266, App	483	481	29.7	1089	14	US-10-176-753-266	Sequence 266, App
411	481	29.7	1089	14	US-10-180-999-266	Sequence 266, App	484	481	29.7	1089	14	US-10-176-917-266	Sequence 266, App
412	481	29.7	1089	14	US-10-183-013-266	Sequence 266, App	485	481	29.7	1089	14	US-10-176-982-266	Sequence 266, App
413	481	29.7	1089	14	US-10-184-612-266	Sequence 266, App	486	481	29.7	1089	14	US-10-179-506-266	Sequence 266, App
414	481	29.7	1089	14	US-10-184-616-266	Sequence 266, App	487	481	29.7	1089	14	US-10-179-513-266	Sequence 266, App
415	481	29.7	1089	14	US-10-184-617-266	Sequence 266, App	488	481	29.7	1089	14	US-10-179-514-266	Sequence 266, App
416	481	29.7	1089	14	US-10-184-622-266	Sequence 266, App	489	481	29.7	1089	14	US-10-183-015-266	Sequence 266, App
417	481	29.7	1089	14	US-10-184-628-266	Sequence 266, App	490	481	29.7	1089	14	US-10-184-615-266	Sequence 266, App
418	481	29.7	1089	14	US-10-184-629-266	Sequence 266, App	491	481	29.7	1089	14	US-10-184-620-266	Sequence 266, App
419	481	29.7	1089	14	US-10-184-630-266	Sequence 266, App	492	481	29.7	1089	14	US-10-184-643-266	Sequence 266, App
420	481	29.7	1089	14	US-10-184-631-266	Sequence 266, App	493	481	29.7	1089	14	US-10-184-656-266	Sequence 266, App
421	481	29.7	1089	14	US-10-184-632-266	Sequence 266, App	494	481	29.7	1089	14	US-10-192-010-266	Sequence 266, App
422	481	29.7	1089	14	US-10-184-636-266	Sequence 266, App	495	481	29.7	1089	14	US-10-205-908-266	Sequence 266, App
423	481	29.7	1089	14	US-10-184-640-266	Sequence 266, App	496	481	29.7	1089	15	US-10-205-506-266	Sequence 266, App
424	481	29.7	1089	14	US-10-184-650-266	Sequence 266, App	497	481	29.7	1089			
425	481	29.7	1089	14	US-10-184-651-266	Sequence 266, App	498	481	29.7	1089			
426	481	29.7	1089	14	US-10-187-588-266	Sequence 266, App	499	481	29.7	1089			
427	481	29.7	1089	14	US-10-187-597-266	Sequence 266, App	500	481	29.7	1089			
428	481	29.7	1089	14	US-10-187-598-266	Sequence 266, App							
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441	481	29.7	1089	14	US-10-187-884-266	Sequence 266, App							
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443	481	29.7	1089	14	US-10-188-769-266	Sequence 266, App							
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447	481	29.7	1089	14	US-10-194-361-266	Sequence 266, App							
448	481	29.7	1089	14	US-10-194-423-266	Sequence 266, App							
449	481	29.7	1089	14	US-10-195-897-266	Sequence 266, App							
450	481	29.7	1089	14	US-10-195-901-266	Sequence 266, App							
451	481	29.7	1089	14	US-10-195-902-266	Sequence 266, App							
452	481	29.7	1089	14	US-10-196-743-266	Sequence 266, App							
453	481	29.7	1089	14	US-10-196-760-266	Sequence 266, App							

ALIGNMENTS

RESULT 1  
US-09-931-836-45  
; Sequence 45, Application US/09931836  
; Publication No. US20030027249A1  
; GENERAL INFORMATION:  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3030R1C1  
; CURRENT APPLICATION NUMBER: US/09/931,836  
; CURRENT FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/085579



; PRIOR APPLICATION NUMBER: PCT/US99/10733  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: PCT/US99/28551  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30720  
; PRIOR FILING DATE: 1999-12-22  
; PRIOR APPLICATION NUMBER: PCT/US00/05601  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: PCT/US00/23522  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: PCT/US00/23328  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US00/34956  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: PCT/US01/17800  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: PCT/US01/19692  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: PCT/US01/21066  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: PCT/US01/21735  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 80  
; SEQ ID NO 45  
; LENGTH: 310  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-931-836-45

Query Match 100.0%; Score 1617; DB 10; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.4e-155;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPEPSAGASSNWTTL 60  
Db |||||  
QY 61 PPPLFSKVIIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIK 120  
Db |||||  
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDSDVIRQAKAAGKRIVIFYGDETWVKLFPKHVEYDGT 180  
Db |||||  
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPNSPILICQKLSEMD 240  
Db |||||  
QY 241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db |||||  
QY 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 2  
US-10-081-056-292  
; Sequence 292, Application US/10081056  
; Publication No. US20040043927A1  
; GENERAL INFORMATION:

; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/112514  
; PRIOR FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: 60/113300  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 60/113430  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/113605  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/113621  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/114140  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/115552  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/116843  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/125774  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/125778  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/125826  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: 60/127035  
; PRIOR FILING DATE: 1999-03-31  
; PRIOR APPLICATION NUMBER: 60/127706  
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; PRIOR APPLICATION NUMBER: 60/129122  
; PRIOR FILING DATE: 1999-04-13  
; PRIOR APPLICATION NUMBER: 60/130359  
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; PRIOR APPLICATION NUMBER: 60/131270  
; PRIOR FILING DATE: 1999-04-27  
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; PRIOR FILING DATE: 1999-05-25  
; PRIOR APPLICATION NUMBER: 60/138166  
; PRIOR FILING DATE: 1999-06-08  
; PRIOR APPLICATION NUMBER: 60/144791  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/146970  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: 60/162506  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: 09/311832  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 09/380142  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: 09/644848  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 09/747259  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 09/816744  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 09/854208  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/854280  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/874503  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: 09/869599  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 09/908,827  
; PRIOR FILING DATE: 2001-07-18

APPLICANT: Baker, Kevin P.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Marsters, Scot A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Ye, Weilan  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS  
FILE REFERENCE: P3235P1C1  
CURRENT APPLICATION NUMBER: US/10/081,056  
CURRENT FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: US 60/219,556  
PRIOR FILING DATE: 2000-07-20  
PRIOR APPLICATION NUMBER: US 60/220,624  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/220,664  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: PCT/US00/20710  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/222,695  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: US 09/643,657  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: PCT/US00/23522  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/230,978  
PRIOR FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: US 60/000,000  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 09/664,610  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 60/242,922  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 09/709,238  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: PCT/US00/30952  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 09/747,259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US 09/767,609  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: US 09/796,498  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/06666  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: US 09/802,706  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: US 09/808,689  
PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: US 09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: US 09/828,366  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: US 09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/854,280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/866,028  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 09/866,034  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: PCT/US01/17092  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 09/870,574  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: PCT/US01/17443  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/00000  
PRIOR FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 383  
SEQ ID NO 292  
LENGTH: 310  
TYPE: PRT  
ORGANISM: Homosapiens  
US-10-081-056-292

Query Match 100.0%; Score 1617; DB 12; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.4e-155;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLSGTGFATCCVAIEVLGIAVFLRGFFPAPVRSSARAHAEGAEPPAPEPSAGASSNWTTL 60  
Db 1 MRLSGTGFATCCVAIEVLGIAVFLRGFFPAPVRSSARAHAEGAEPPAPEPSAGASSNWTTL 60  
QY 61 PPPLFSKWIVLIDALRDDVFVFGSGKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120  
Db 61 PPPLFSKWIVLIDALRDDVFVFGSGKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120  
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAAGKRIVFYGDETWVLPKHFVEYDGT 180  
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAAGKRIVFYGDETWVLPKHFVEYDGT 180  
QY 181 TSFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPNPLIGQKLSMD 240  
Db 181 TSFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPNPLIGQKLSMD 240  
QY 241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db 241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
QY 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 3  
US-10-219-535-118  
Sequence 118, Application US/10219535  
Publication No. US20040044179A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530P1C60  
CURRENT APPLICATION NUMBER: US/10/219,535  
CURRENT FILING DATE: 2002-08-14  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 118  
LENGTH: 310  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-219-535-118

Query Match 100.0%; Score 1617; DB 12; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.4e-155;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRLSGTFFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60  
Db 1 MRLSGTFFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60  
QY 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120  
Db 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120  
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPPKHFEYDGT 180  
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPPKHFEYDGT 180  
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPN SPLIGQKLSMD 240  
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPN SPLIGQKLSMD 240  
QY 241 SVLMKIHTSLOSKERETPLPNNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db 241 SVLMKIHTSLOSKERETPLPNNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
QY 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 4  
US-10-232-230-118  
Sequence 118, Application US/10232230  
Publication No. US20040044180A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530P1C103  
CURRENT APPLICATION NUMBER: US/10/232,230  
CURRENT FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 118  
LENGTH: 310  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-232-230-118

Query Match 100.0%; Score 1617; DB 12; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.4e-155;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRLSGTFFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60  
Db 1 MRLSGTFFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60  
QY 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120  
Db 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120  
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPPKHFEYDGT 180  
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPPKHFEYDGT 180  
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPN SPLIGQKLSMD 240  
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPN SPLIGQKLSMD 240  
QY 241 SVLMKIHTSLOSKERETPLPNNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db 241 SVLMKIHTSLOSKERETPLPNNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
QY 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 5  
US-10-063-745-140  
Sequence 140, Application US/10063745



```

; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-745-140

Query Match      100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60
Db      1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60

QY      61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTTILVEKGASHSFVAEAKPPTVTMPRIK 120
Db      61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTTILVEKGASHSFVAEAKPPTVTMPRIK 120

QY      121 ALMTGSLPGFVDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180
Db      121 ALMTGSLPGFVDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180

QY      181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYGLDGHIGHISGPNPLIGQKLSMD 240
Db      181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYGLDGHIGHISGPNPLIGQKLSMD 240

QY      241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
Db      241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300

QY      301 GDIRHPKHVQ 310
Db      301 GDIRHPKHVQ 310

RESULT 6
US-10-063-512-140
; Sequence 140, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; US-10-063-512-140

Query Match      100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60
Db      1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60

QY      61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTTILVEKGASHSFVAEAKPPTVTMPRIK 120
Db      61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTTILVEKGASHSFVAEAKPPTVTMPRIK 120

QY      121 ALMTGSLPGFVDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180
Db      121 ALMTGSLPGFVDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180

QY      181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYGLDGHIGHISGPNPLIGQKLSMD 240
Db      181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYGLDGHIGHISGPNPLIGQKLSMD 240

QY      241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
Db      241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300

QY      301 GDIRHPKHVQ 310
Db      301 GDIRHPKHVQ 310

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; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-512-140

Query Match      100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60
Db      1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60

QY      61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTTILVEKGASHSFVAEAKPPTVTMPRIK 120
Db      61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTTILVEKGASHSFVAEAKPPTVTMPRIK 120

QY      121 ALMTGSLPGFVDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180
Db      121 ALMTGSLPGFVDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180

QY      181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYGLDGHIGHISGPNPLIGQKLSMD 240
Db      181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYGLDGHIGHISGPNPLIGQKLSMD 240

QY      241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
Db      241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300

QY      301 GDIRHPKHVQ 310
Db      301 GDIRHPKHVQ 310

RESULT 7
US-10-063-513-140
; Sequence 140, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-513-140

Query Match      100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60
Db      1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60

QY      61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTTILVEKGASHSFVAEAKPPTVTMPRIK 120
Db      61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTTILVEKGASHSFVAEAKPPTVTMPRIK 120

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Db 61 PPPLFSKVVIVLIDALRDDDFVFGSKGVKFMPTTTLVEKGASHSFVAEAKPPTVTMPRIK 120  
Qy 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPHFVEYDGT 180  
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPHFVEYDGT 180  
Qy 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNPLIGQKLSMD 240  
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNPLIGQKLSMD 240  
Qy 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Qy 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 8

US-10-063-515-140  
; Sequence 140, Application US/10063515  
; Publication No. US20030018173A1  
; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,515  
; CURRENT FILING DATE: 2002-05-01  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 140  
; LENGTH: 310  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-515-140

Query Match 100.0%; Score 1617; DB 12; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.4e-155;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60  
Db 1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60  
Qy 61 PPPLFSKVVIVLIDALRDDDFVFGSKGVKFMPTTTLVEKGASHSFVAEAKPPTVTMPRIK 120  
Db 61 PPPLFSKVVIVLIDALRDDDFVFGSKGVKFMPTTTLVEKGASHSFVAEAKPPTVTMPRIK 120  
Qy 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPHFVEYDGT 180  
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPHFVEYDGT 180  
Qy 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNPLIGQKLSMD 240  
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNPLIGQKLSMD 240  
Qy 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Qy 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 9

US-10-063-549-140  
; Sequence 140, Application US/10063549  
; Publication No. US20030027986A1  
; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,549  
; CURRENT FILING DATE: 2002-05-02  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 140  
; LENGTH: 310  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-549-140

Query Match 100.0%; Score 1617; DB 12; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.4e-155;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60  
Db 1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTL 60  
Qy 61 PPPLFSKVVIVLIDALRDDDFVFGSKGVKFMPTTTLVEKGASHSFVAEAKPPTVTMPRIK 120  
Db 61 PPPLFSKVVIVLIDALRDDDFVFGSKGVKFMPTTTLVEKGASHSFVAEAKPPTVTMPRIK 120  
Qy 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPHFVEYDGT 180  
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPHFVEYDGT 180  
Qy 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNPLIGQKLSMD 240  
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNPLIGQKLSMD 240  
Qy 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Qy 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 10

US-10-063-569-140  
; Sequence 140, Application US/10063569  
; Publication No. US20030018168A1  
; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-569-140

Query Match 100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTL 60
Db 1 MRLSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSGVKFMPYTTTLYVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDDFVFGSGVKFMPYTTTLYVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGPNPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGPNPLIGQKLSMD 240
QY 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

RESULT 11
US-10-063-551-140
; Sequence 140, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-551-140

Query Match 100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTL 60

Db 1 MRLSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSGVKFMPYTTTLYVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDDFVFGSGVKFMPYTTTLYVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGPNPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGPNPLIGQKLSMD 240
QY 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

RESULT 12
US-10-063-555-140
; Sequence 140, Application US/10063555
; Publication No. US20030065143A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,555
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-555-140

Query Match 100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTL 60
Db 1 MRLSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSGVKFMPYTTTLYVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDDFVFGSGVKFMPYTTTLYVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIROAKAAGKRIVFYGDETWVKLFPKHFEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGPNPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGPNPLIGQKLSMD 240
QY 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300



Db 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
QY 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 13

US-10-063-563-140  
; Sequence 140, Application US/10063563  
; Publication No. US20030060602A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,563  
; CURRENT FILING DATE: 2002-05-02  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 140  
; LENGTH: 310  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-563-140

Query Match 100.0%; Score 1617; DB 12; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.4e-155;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLSGTGFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPEPSAGASSNWTTL 60  
Db 1 MRLSGTGFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPEPSAGASSNWTTL 60  
QY 61 PPPLFSKVVIIVLIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120  
Db 61 PPPLFSKVVIIVLIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120  
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDETWTWVCLFPKHFEYDGT 180  
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDETWTWVCLFPKHFEYDGT 180  
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHSGPNSPLIGQKLSMD 240  
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHSGPNSPLIGQKLSMD 240  
QY 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
QY 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 14

US-10-063-594-140  
; Sequence 140, Application US/10063594  
; Publication No. US20030065161A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,594  
; CURRENT FILING DATE: 2002-05-30  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 140  
; LENGTH: 310  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-594-140

Query Match 100.0%; Score 1617; DB 12; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.4e-155;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLSGTGFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPEPSAGASSNWTTL 60  
Db 1 MRLSGTGFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPEPSAGASSNWTTL 60  
QY 61 PPPLFSKVVIIVLIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120  
Db 61 PPPLFSKVVIIVLIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK 120  
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDETWTWVCLFPKHFEYDGT 180  
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDETWTWVCLFPKHFEYDGT 180  
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHSGPNSPLIGQKLSMD 240  
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHSGPNSPLIGQKLSMD 240  
QY 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
Db 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300  
QY 301 GDIRHPKHVQ 310  
Db 301 GDIRHPKHVQ 310

RESULT 15

US-10-063-553-140  
; Sequence 140, Application US/10063553  
; Publication No. US20030045684A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,553  
; CURRENT FILING DATE: 2002-05-02  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 140  
; LENGTH: 310  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-553-140

Query Match		100.0%;	Score 1617;	DB 12;	Length 310;
Best Local Similarity		100.0%;	Pred. No. 1.4e-155;		
Matches 310;	Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
Qy	1	MRLSGTGFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPAPSAGASSNWTTL	60		
Db	1	MRLSGTGFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPAPSAGASSNWTTL	60		
Qy	61	PPPLFSKVIVLIDALRDDVFVFGSKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK	120		
Db	61	PPPLFSKVIVLIDALRDDVFVFGSKGVKFMPTTYTLVEKGASHSFVAEAKPPTVTMPRIK	120		
Qy	121	ALMTGSLPGFVDVIRNLNSPALLEDSVIRQAKAGKRIVFYGDETWVKLFPKHFEYDGT	180		
Db	121	ALMTGSLPGFVDVIRNLNSPALLEDSVIRQAKAGKRIVFYGDETWVKLFPKHFEYDGT	180		
Qy	181	TSFVSDYTEVDNNTVRHLDKVLKRGDWDILILHVLGLDHHIGHISGPNSPILIGQKLSMD	240		
Db	181	TSFVSDYTEVDNNTVRHLDKVLKRGDWDILILHVLGLDHHIGHISGPNSPILIGQKLSMD	240		
Qy	241	SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP	300		
Db	241	SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP	300		
Qy	301	GDIRHPKHVQ	310		
Db	301	GDIRHPKHVQ	310		

Search completed: August 2, 2004, 16:31:39  
Job time : 47 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:27:33 ; Search time 19 Seconds  
(without alignments)  
842.318 Million cell updates/sec

Title: US-10-036-150-45  
Perfect score: 1617  
Sequence: 1 MRLSGTGFATCCVAIEVLGI.....LISSAFERKPGDIRHPKHVQ 310

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	220.5	13.6	185	4	US-09-621-976-4112
2	170	10.5	287	4	US-09-252-991A-21605
3	148	9.2	275	4	US-09-540-236-2033
4	139	8.6	355	2	US-09-014-969-19
5	127	7.9	438	3	US-09-187-331-2
6	127	7.9	438	4	US-09-470-946-2
7	101	6.2	873	3	US-09-187-331-6
8	101	6.2	873	4	US-09-470-946-6
9	101	6.2	873	4	US-09-438-906-2
10	101	6.2	873	4	US-09-438-906-4
11	101	6.2	925	2	US-08-392-946-1
12	101	6.2	925	2	US-08-504-169-1
13	101	6.2	925	5	PCT-US94-14893-1
14	99	6.1	230	4	US-09-107-532A-4717
15	96.5	6.0	2109	3	US-08-646-695-6
16	96.5	6.0	2109	5	PCT-US96-06053-6
17	95	5.9	311	3	US-09-277-716-18
18	95	5.9	311	4	US-09-609-161B-18
19	94.5	5.8	686	4	US-09-252-991A-26437
20	92	5.7	331	2	US-08-986-217-7
21	92	5.7	333	4	US-09-562-737-5
22	92	5.7	620	3	US-09-000-145-5
23	89.5	5.5	796	3	US-08-961-083-56
24	89.5	5.5	796	4	US-09-536-784-56
25	89	5.5	1245	4	US-09-543-681A-5592
26	88.5	5.5	470	4	US-09-266-965-118
27	88.5	5.5	819	4	US-09-468-656A-8
28	87.5	5.4	911	1	US-08-596-985-2
29	87	5.4	311	3	US-09-330-317B-2
30	87	5.4	311	4	US-09-808-589A-2
31	87	5.4	339	3	US-09-330-317B-4
32	87	5.4	339	3	US-09-330-317B-10
33	87	5.4	339	3	US-09-330-317B-12
34	87	5.4	339	3	US-09-330-317B-14
35	87	5.4	339	3	US-09-330-317B-16
36	87	5.4	339	4	US-09-808-589A-4
37	87	5.4	339	4	US-09-808-589A-10
38	87	5.4	339	4	US-09-808-589A-12
39	87	5.4	339	4	US-09-808-589A-14
40	87	5.4	339	4	US-09-808-589A-16
41	86	5.3	657	4	US-09-252-991A-27358
42	86	5.3	861	1	US-08-346-455B-67
43	86	5.3	861	3	US-08-977-221-67
44	86	5.3	861	4	US-09-483-831B-67
45	86	5.3	861	4	US-09-784-316-2
46	86	5.3	861	5	PCT-US95-06613-67
47	85	5.3	1098	1	US-08-290-301-82
48	85	5.3	1098	4	US-09-013-598-82
49	84.5	5.2	368	3	US-08-972-902-2
50	84.5	5.2	368	4	US-09-520-207-2
51	84.5	5.2	368	4	US-10-136-253-2
52	83.5	5.2	903	1	US-08-750-532-1
53	83.5	5.2	1398	1	US-08-750-532-9
54	83.5	5.2	1398	3	US-08-894-818B-8
55	83.5	5.2	1398	4	US-09-445-472-6
56	82.5	5.1	266	4	US-09-489-039A-8199
57	82.5	5.1	575	4	US-09-071-035-296
58	82.5	5.1	601	4	US-09-071-035-294
59	82	5.1	344	4	US-09-252-991A-31357
60	82	5.1	1091	3	US-09-306-595C-7
61	82	5.1	1091	4	US-09-925-388-7
62	81.5	5.0	502	4	US-09-252-991A-30007
63	81.5	5.0	521	4	US-09-328-352-5423
64	81	5.0	235	4	US-09-107-532A-6882
65	81	5.0	313	3	US-09-347-803-6
66	81	5.0	360	4	US-09-252-991A-19088
67	81	5.0	1394	4	US-09-845-917A-57
68	81	5.0	1449	4	US-09-845-917A-58
69	81	5.0	1528	4	US-09-845-917A-3
70	81	5.0	1583	4	US-09-845-917A-4
71	81	5.0	1890	4	US-09-004-838-88
72	80	4.9	604	4	US-09-391-104-30
73	80	4.9	1817	4	US-09-004-838-125
74	79.5	4.9	911	4	US-08-461-562B-2
75	79.5	4.9	986	4	US-09-403-618A-5
76	79	4.9	427	4	US-08-065-844A-2
77	79	4.9	444	4	US-09-328-352-7043
78	78.5	4.9	287	4	US-09-252-991A-19272
79	78.5	4.9	338	4	US-09-489-039A-10172
80	78.5	4.9	364	4	US-09-417-485D-46
81	78.5	4.9	388	4	US-09-331-568A-4
82	78.5	4.9	388	4	US-09-331-568A-29
83	78.5	4.9	409	4	US-09-540-236-3384
84	78.5	4.9	775	2	US-08-714-677-4
85	78.5	4.9	775	2	US-08-393-540-4
86	78.5	4.9	775	2	US-08-714-537-4
87	78	4.8	437	1	US-08-136-119-4
88	78	4.8	437	2	US-08-723-415B-13
89	78	4.8	437	2	US-08-481-814A-6
90	78	4.8	437	3	US-08-801-092-1
91	78	4.8	437	3	US-09-189-627A-13
92	78	4.8	437	4	US-09-242-737-2
93	78	4.8	437	4	US-09-315-113-1
94	78	4.8	437	4	US-09-710-861-13
95	78	4.8	476	2	US-08-139-937-14
96	78	4.8	476	5	PCT-US93-11310-14
97	78	4.8	607	3	US-09-000-041A-2
98	77.5	4.8	392	4	US-09-134-000C-6542
99	77.5	4.8	521	4	US-09-134-001C-4290
100	77.5	4.8	582	3	US-08-906-865-3



101	77.5	4.8	582	4	US-09-129-668-3	Sequence 3, Appli	174	73.5	4.5	511	4	US-09-328-352-6176	Sequence 6176, Ap
102	77.5	4.8	865	4	US-09-281-766-19	Sequence 19, Appl	175	73.5	4.5	517	4	US-09-134-001C-5444	Sequence 5444, Ap
103	77	4.8	213	4	US-09-540-236-2742	Sequence 2742, Ap	176	73.5	4.5	526	4	US-09-252-991A-21748	Sequence 21748, A
104	77	4.8	412	2	US-08-414-938A-4	Sequence 4, Appli	177	73.5	4.5	565	4	US-09-489-039A-10676	Sequence 10676, A
105	77	4.8	541	4	US-09-614-912-66	Sequence 66, Appl	178	73.5	4.5	706	4	US-09-134-001C-4908	Sequence 4908, Ap
106	76.5	4.7	170	3	US-09-130-663-2	Sequence 2, Appli	179	73	4.5	317	4	US-09-252-991A-29954	Sequence 29954, A
107	76.5	4.7	170	3	US-09-432-335-2	Sequence 2, Appli	180	73	4.5	344	2	US-08-690-493-1	Sequence 1, Appli
108	76.5	4.7	170	3	US-09-614-022-2	Sequence 2, Appli	181	73	4.5	650	4	US-09-134-001C-4444	Sequence 4444, Ap
109	76.5	4.7	237	4	US-09-134-001C-5631	Sequence 5631, Ap	182	73	4.5	696	4	US-09-107-532A-5205	Sequence 5205, Ap
110	76.5	4.7	711	4	US-09-485-737B-90	Sequence 90, Appl	183	73	4.5	863	4	US-09-894-927B-9	Sequence 9, Appli
111	76.5	4.7	763	4	US-09-328-352-4406	Sequence 4406, Ap	184	73	4.5	1024	4	US-09-562-737-46	Sequence 46, Appl
112	76.5	4.7	1565	4	US-08-851-567B-59	Sequence 59, Appl	185	72.5	4.5	223	1	US-08-430-633-1	Sequence 1, Appli
113	76	4.7	306	4	US-09-543-681A-7494	Sequence 7494, Ap	186	72.5	4.5	223	2	US-08-936-854-1	Sequence 1, Appli
114	76	4.7	437	1	US-07-882-711-2	Sequence 2, Appli	187	72.5	4.5	303	3	US-08-928-361B-7	Sequence 7, Appli
115	76	4.7	437	2	US-08-462-174-2	Sequence 2, Appli	188	72.5	4.5	303	4	US-09-588-995A-7	Sequence 7, Appli
116	76	4.7	581	4	US-09-252-991A-17734	Sequence 17734, A	189	72.5	4.5	326	2	US-08-986-217-3	Sequence 3, Appli
117	76	4.7	620	3	US-09-000-145-3	Sequence 3, Appli	190	72.5	4.5	369	2	US-08-596-291-4	Sequence 4, Appli
118	76	4.7	718	4	US-09-107-532A-5234	Sequence 5234, Ap	191	72.5	4.5	369	3	US-09-100-804-4	Sequence 4, Appli
119	76	4.7	935	2	US-08-152-721B-2	Sequence 2, Appli	192	72.5	4.5	369	4	US-09-489-039A-10540	Sequence 10540, A
120	76	4.7	1289	2	US-08-853-659A-51	Sequence 51, Appl	193	72.5	4.5	369	5	PCT-US94-09943-4	Sequence 4, Appli
121	76	4.7	2366	1	US-08-480-604A-10	Sequence 10, Appl	194	72.5	4.5	393	4	US-09-543-681A-5865	Sequence 5865, Ap
122	76	4.7	2366	2	US-08-405-496A-10	Sequence 10, Appl	195	72.5	4.5	416	4	US-09-543-681A-4386	Sequence 4386, Ap
123	76	4.7	2366	3	US-08-915-136-10	Sequence 10, Appl	196	72.5	4.5	429	4	US-09-489-039A-13738	Sequence 13738, A
124	76	4.7	2366	4	US-08-957-310-10	Sequence 10, Appl	197	72.5	4.5	479	4	US-09-489-039A-11164	Sequence 11164, A
125	76	4.7	2366	4	US-10-011-366-10	Sequence 10, Appl	198	72.5	4.5	499	4	US-09-489-039A-9208	Sequence 9208, Ap
126	76	4.7	2366	4	US-09-084-517-10	Sequence 10, Appl	199	72.5	4.5	550	4	US-09-107-532A-5564	Sequence 5564, Ap
127	75.5	4.7	333	4	US-09-562-737-2	Sequence 2, Appli	200	72.5	4.5	575	1	US-07-683-957B-2	Sequence 2, Appli
128	75.5	4.7	472	4	US-09-625-188-6	Sequence 6, Appli	201	72.5	4.5	579	4	US-09-543-681A-5296	Sequence 5296, Ap
129	75.5	4.7	512	2	US-08-557-122A-33	Sequence 33, Appl	202	72.5	4.5	616	3	US-09-136-574A-47	Sequence 47, Appl
130	75.5	4.7	512	4	US-09-262-666-33	Sequence 33, Appl	203	72.5	4.5	791	4	US-09-107-532A-6065	Sequence 6065, Ap
131	75	4.6	441	4	US-09-328-352-5114	Sequence 5114, Ap	204	72.5	4.5	871	2	US-08-775-009-35	Sequence 35, Appl
132	75	4.6	485	4	US-09-489-039A-10554	Sequence 10554, A	205	72.5	4.5	885	2	US-08-500-857A-8	Sequence 8, Appli
133	75	4.6	496	4	US-09-489-039A-7787	Sequence 7787, Ap	206	72.5	4.5	1426	3	US-09-136-574A-43	Sequence 43, Appl
134	75	4.6	547	1	US-08-785-048-3	Sequence 3, Appli	207	72.5	4.5	1837	3	US-08-928-361B-5	Sequence 5, Appli
135	75	4.6	547	2	US-08-996-799-3	Sequence 3, Appli	208	72.5	4.5	1837	4	US-09-588-995A-5	Sequence 5, Appli
136	75	4.6	553	1	US-08-785-048-2	Sequence 2, Appli	209	72.5	4.5	2319	1	US-08-212-133A-8	Sequence 8, Appli
137	75	4.6	553	2	US-08-996-799-2	Sequence 2, Appli	210	72.5	4.5	2319	1	US-08-474-503-6	Sequence 6, Appli
138	75	4.6	582	4	US-09-252-991A-29341	Sequence 29341, A	211	72.5	4.5	2319	2	US-08-670-707A-6	Sequence 6, Appli
139	75	4.6	976	2	US-08-449-645A-18	Sequence 18, Appl	212	72.5	4.5	2319	3	US-09-037-601-6	Sequence 6, Appli
140	75	4.6	976	2	US-08-702-367A-18	Sequence 18, Appl	213	72.5	4.5	2319	4	US-09-315-179-6	Sequence 6, Appli
141	75	4.6	976	5	PCT-US95-04681-18	Sequence 18, Appl	214	72.5	4.5	2319	4	US-09-523-656-28	Sequence 28, Appl
142	74.5	4.6	250	4	US-09-252-991A-32751	Sequence 32751, A	215	72.5	4.5	2319	5	PCT-US94-13200-6	Sequence 6, Appli
143	74.5	4.6	474	4	US-09-134-001C-3241	Sequence 3241, Ap	216	72.5	4.5	3072	3	US-09-413-814-93	Sequence 93, Appl
144	74.5	4.6	513	1	US-08-403-866-1	Sequence 1, Appli	217	72.5	4.5	3079	3	US-09-413-814-80	Sequence 80, Appl
145	74.5	4.6	599	4	US-09-773-426A-7	Sequence 7, Appli	218	72	4.5	182	3	US-09-338-907-133	Sequence 133, App
146	74.5	4.6	715	2	US-08-484-993B-10	Sequence 10, Appl	219	72	4.5	182	4	US-09-218-207-133	Sequence 133, App
147	74.5	4.6	715	2	US-08-484-158B-10	Sequence 10, Appl	220	72	4.5	324	2	US-08-671-320-11	Sequence 11, Appl
148	74.5	4.6	715	2	US-08-484-596A-10	Sequence 10, Appl	221	72	4.5	324	2	US-08-868-577-11	Sequence 11, Appl
149	74.5	4.6	715	2	US-08-480-150A-10	Sequence 10, Appl	222	72	4.5	324	4	US-09-207-914-11	Sequence 11, Appl
150	74.5	4.6	715	3	US-08-458-731-10	Sequence 10, Appl	223	72	4.5	451	3	US-09-371-913A-9	Sequence 9, Appli
151	74.5	4.6	715	3	US-08-149-223A-10	Sequence 10, Appl	224	72	4.5	451	4	US-09-967-805-9	Sequence 9, Appli
152	74.5	4.6	879	4	US-09-107-532A-4679	Sequence 4679, Ap	225	72	4.5	516	2	US-08-676-166A-7	Sequence 7, Appli
153	74.5	4.6	1041	1	US-08-220-151-4	Sequence 4, Appli	226	72	4.5	588	4	US-09-252-991A-24185	Sequence 24185, A
154	74.5	4.6	1041	1	US-08-413-118-4	Sequence 4, Appli	227	72	4.5	638	4	US-09-489-039A-8996	Sequence 8996, Ap
155	74.5	4.6	1041	3	US-08-473-446-4	Sequence 4, Appli	228	72	4.5	713	4	US-09-059-584-49	Sequence 49, Appl
156	74.5	4.6	1708	4	US-09-462-606-2	Sequence 2, Appli	229	72	4.5	1088	4	US-09-233-857-13	Sequence 13, Appl
157	74	4.6	355	4	US-09-574-377-12	Sequence 12, Appl	230	72	4.5	1099	4	US-09-442-100-2	Sequence 2, Appli
158	74	4.6	460	4	US-09-266-965-126	Sequence 126, App	231	72	4.5	1099	4	US-08-939-106-2	Sequence 2, Appli
159	74	4.6	607	3	US-09-211-704A-10	Sequence 10, Appl	232	72	4.5	1099	4	US-09-442-102-2	Sequence 2, Appli
160	74	4.6	612	1	US-08-344-695-2	Sequence 2, Appli	233	72	4.5	1203	4	US-09-075-272-4	Sequence 4, Appli
161	74	4.6	709	4	US-09-668-673B-3	Sequence 3, Appli	234	72	4.5	1341	4	US-09-252-991A-26785	Sequence 26785, A
162	74	4.6	715	4	US-09-107-532A-4219	Sequence 4219, Ap	235	72	4.5	2618	3	US-09-413-814-28	Sequence 28, Appl
163	74	4.6	851	4	US-09-623-326-43	Sequence 43, Appl	236	71.5	4.4	223	4	US-09-540-236-3044	Sequence 3044, Ap
164	74	4.6	946	4	US-09-252-991A-18989	Sequence 18989, A	237	71.5	4.4	333	4	US-09-562-737-6	Sequence 6, Appli
165	74	4.6	953	2	US-08-500-857A-2	Sequence 2, Appli	238	71.5	4.4	348	4	US-09-198-452A-38	Sequence 38, Appl
166	74	4.6	1704	4	US-09-324-812A-2	Sequence 2, Appli	239	71.5	4.4	355	4	US-09-501-115-12	Sequence 12, Appl
167	74	4.6	2343	3	US-09-324-867-2	Sequence 2, Appli	240	71.5	4.4	381	4	US-09-489-039A-10807	Sequence 10807, A
168	74	4.6	3546	4	US-09-679-279-13	Sequence 13, Appl	241	71.5	4.4	397	4	US-09-252-991A-23159	Sequence 23159, A
169	73.5	4.5	323	3	US-09-029-213B-25	Sequence 25, Appl	242	71.5	4.4	421	4	US-09-252-991A-31469	Sequence 31469, A
170	73.5	4.5	383	1	US-08-464-523B-31	Sequence 31, Appl	243	71.5	4.4	436	3	US-08-669-378-12	Sequence 12, Appl
171	73.5	4.5	408	4	US-09-252-991A-33131	Sequence 33131, A	244	71.5	4.4	443	2	US-08-935-450-6	Sequence 6, Appli
172	73.5	4.5	436	3	US-08-669-378-4	Sequence 4, Appli	245	71.5	4.4	443	4	US-08-952-899-2	Sequence 2, Appli
173	73.5	4.5	503	4	US-09-562-737-68	Sequence 68, Appl	246	71.5	4.4	443	4	US-09-338-123-6	Sequence 6, Appli

247	71.5	4.4	562	3	US-09-211-704A-4	Sequence 4, Appli	Sequence 4, Appli	320	70.5	4.4	353	3	US-08-482-212-2	Sequence 2, Appli
248	71.5	4.4	567	4	US-09-489-039A-10840	Sequence 10840, A	Sequence 10840, A	321	70.5	4.4	353	3	US-08-471-045-55	Sequence 55, Appl
249	71.5	4.4	576	3	US-09-347-801-19	Sequence 19, Appl	Sequence 19, Appl	322	70.5	4.4	353	3	US-08-469-712A-55	Sequence 55, Appl
250	71.5	4.4	663	1	US-08-441-139-7	Sequence 7, Appli	Sequence 7, Appli	323	70.5	4.4	353	3	US-08-999-927-2	Sequence 2, Appli
251	71.5	4.4	867	4	US-09-275-252A-11	Sequence 11, Appl	Sequence 11, Appl	324	70.5	4.4	353	3	US-08-999-927-6	Sequence 6, Appli
252	71.5	4.4	850	4	US-09-540-236-2184	Sequence 2184, Ap	Sequence 2184, Ap	325	70.5	4.4	353	4	US-08-461-819-2	Sequence 2, Appli
253	71.5	4.4	877	4	US-09-252-991A-25547	Sequence 25547, A	Sequence 25547, A	326	70.5	4.4	353	4	US-08-461-819-6	Sequence 6, Appli
254	71.5	4.4	1019	4	US-09-543-681A-4447	Sequence 4447, Ap	Sequence 4447, Ap	327	70.5	4.4	353	4	US-08-446-871-55	Sequence 55, Appl
255	71.5	4.4	1024	4	US-09-562-737-48	Sequence 48, Appl	Sequence 48, Appl	328	70.5	4.4	353	4	US-08-468-910-55	Sequence 55, Appl
256	71.5	4.4	1447	3	US-09-041-886-25	Sequence 25, Appl	Sequence 25, Appl	329	70.5	4.4	353	4	US-08-761-907-55	Sequence 55, Appl
257	71.5	4.4	1447	5	PCT-US94-05277-2	Sequence 2, Appli	Sequence 2, Appli	330	70.5	4.4	353	4	US-09-872-702-13	Sequence 13, Appl
258	71.5	4.4	1596	4	US-09-328-352-5542	Sequence 5542, Ap	Sequence 5542, Ap	331	70.5	4.4	353	5	PCT-US94-08806-19	Sequence 29, Appl
259	71	4.4	198	4	US-09-543-681A-7727	Sequence 7727, Ap	Sequence 7727, Ap	332	70.5	4.4	353	5	PCT-US94-08806-29	Sequence 29, Appl
260	71	4.4	246	4	US-09-252-991A-30011	Sequence 30011, A	Sequence 30011, A	333	70.5	4.4	353	5	PCT-US95-01829-2	Sequence 2, Appli
261	71	4.4	397	1	US-07-956-697B-5	Sequence 5, Appli	Sequence 5, Appli	334	70.5	4.4	353	5	PCT-US95-01829-6	Sequence 6, Appli
262	71	4.4	397	1	US-08-263-098-5	Sequence 5, Appli	Sequence 5, Appli	335	70.5	4.4	353	5	PCT-US95-14932-4	Sequence 4, Appli
263	71	4.4	398	4	US-09-107-532A-3810	Sequence 3810, Ap	Sequence 3810, Ap	336	70.5	4.4	353	5	PCT-US95-16626-4	Sequence 4, Appli
264	71	4.4	451	4	US-09-252-991A-32664	Sequence 32664, A	Sequence 32664, A	337	70.5	4.4	353	5	PCT-US95-16626-6	Sequence 6, Appli
265	71	4.4	462	4	US-08-630-915A-38	Sequence 38, Appl	Sequence 38, Appl	338	70.5	4.4	436	3	US-08-669-378-2	Sequence 2, Appli
266	71	4.4	480	3	US-09-108-020-6	Sequence 6, Appli	Sequence 6, Appli	339	70.5	4.4	441	2	US-08-491-835-4	Sequence 4, Appli
267	71	4.4	514	4	US-09-266-965-116	Sequence 116, App	Sequence 116, App	340	70.5	4.4	441	3	US-08-946-092A-4	Sequence 4, Appli
268	71	4.4	662	3	US-09-232-191-11	Sequence 11, Appl	Sequence 11, Appl	341	70.5	4.4	441	3	US-09-172-062-4	Sequence 4, Appli
269	71	4.4	662	3	US-09-232-200-11	Sequence 11, Appl	Sequence 11, Appl	342	70.5	4.4	441	4	US-09-301-520D-4	Sequence 4, Appli
270	71	4.4	662	3	US-09-232-200-96	Sequence 96, Appl	Sequence 96, Appl	343	70.5	4.4	441	5	PCT-US94-00685-4	Sequence 4, Appli
271	71	4.4	662	4	US-09-232-197-11	Sequence 11, Appl	Sequence 11, Appl	344	70.5	4.4	441	5	US-09-504-358-2	Sequence 2, Appli
272	71	4.4	662	4	US-09-232-197-96	Sequence 96, Appl	Sequence 96, Appl	345	70.5	4.4	458	4	US-09-954-314-2	Sequence 2, Appli
273	71	4.4	662	4	US-09-232-201-11	Sequence 11, Appl	Sequence 11, Appl	346	70.5	4.4	513	4	US-09-107-532A-5261	Sequence 5261, Ap
274	71	4.4	662	4	US-09-232-201-96	Sequence 96, Appl	Sequence 96, Appl	347	70.5	4.4	529	1	US-08-178-477B-32	Sequence 32, Appl
275	71	4.4	662	4	US-09-232-195-11	Sequence 11, Appl	Sequence 11, Appl	348	70.5	4.4	529	4	US-09-304-121-2	Sequence 2, Appli
276	71	4.4	662	4	US-09-232-195-96	Sequence 96, Appl	Sequence 96, Appl	349	70.5	4.4	569	4	US-09-107-532A-6689	Sequence 6689, Ap
277	71	4.4	689	3	US-09-232-200-73	Sequence 73, Appl	Sequence 73, Appl	350	70.5	4.4	648	4	US-09-198-452A-594	Sequence 594, App
278	71	4.4	689	4	US-09-232-197-73	Sequence 73, Appl	Sequence 73, Appl	351	70.5	4.4	702	2	US-08-867-941-25	Sequence 25, Appl
279	71	4.4	689	4	US-09-232-201-73	Sequence 73, Appl	Sequence 73, Appl	352	70.5	4.4	702	3	US-08-613-009A-9	Sequence 9, Appli
280	71	4.4	689	4	US-09-232-195-73	Sequence 73, Appl	Sequence 73, Appl	353	70.5	4.4	702	3	US-09-074-658-25	Sequence 25, Appl
281	71	4.4	947	4	US-09-252-991A-21398	Sequence 21398, A	Sequence 21398, A	354	70.5	4.4	702	4	US-08-778-570B-11	Sequence 11, Appl
282	71	4.4	1118	3	US-09-379-523-3	Sequence 3, Appli	Sequence 3, Appli	355	70.5	4.4	702	4	US-09-059-584-11	Sequence 11, Appl
283	70.5	4.4	253	4	US-09-328-352-8134	Sequence 8134, Ap	Sequence 8134, Ap	356	70.5	4.4	706	4	US-09-059-584-46	Sequence 46, Appl
284	70.5	4.4	279	4	US-09-134-001C-4878	Sequence 4878, Ap	Sequence 4878, Ap	357	70.5	4.4	783	4	US-09-513-783A-176	Sequence 176, App
285	70.5	4.4	326	2	US-08-997-080-43	Sequence 43, Appl	Sequence 43, Appl	358	70.5	4.4	829	1	US-08-346-455B-34	Sequence 34, Appl
286	70.5	4.4	326	2	US-08-997-362-43	Sequence 43, Appl	Sequence 43, Appl	359	70.5	4.4	829	3	US-08-977-221-34	Sequence 34, Appl
287	70.5	4.4	326	3	US-08-873-970-43	Sequence 43, Appl	Sequence 43, Appl	360	70.5	4.4	829	4	US-09-483-831B-34	Sequence 34, Appl
288	70.5	4.4	326	3	US-09-095-855-43	Sequence 43, Appl	Sequence 43, Appl	361	70.5	4.4	829	5	PCT-US95-06613-34	Sequence 34, Appl
289	70.5	4.4	326	3	US-08-705-347A-43	Sequence 43, Appl	Sequence 43, Appl	362	70.5	4.4	915	1	US-08-346-455B-69	Sequence 69, Appl
290	70.5	4.4	326	4	US-09-324-542-43	Sequence 43, Appl	Sequence 43, Appl	363	70.5	4.4	915	3	US-08-977-221-69	Sequence 69, Appl
291	70.5	4.4	326	4	US-09-205-426-43	Sequence 43, Appl	Sequence 43, Appl	364	70.5	4.4	915	4	US-09-483-831B-69	Sequence 69, Appl
292	70.5	4.4	326	4	US-09-200-643-43	Sequence 43, Appl	Sequence 43, Appl	365	70.5	4.4	915	5	PCT-US95-06613-69	Sequence 69, Appl
293	70.5	4.4	328	3	US-08-875-533-37	Sequence 37, Appl	Sequence 37, Appl	366	70.5	4.4	990	4	US-09-252-991A-22792	Sequence 22792, A
294	70.5	4.4	332	3	US-08-875-533-1	Sequence 1, Appli	Sequence 1, Appli	367	70.5	4.4	1382	2	US-08-737-715-2	Sequence 2, Appli
295	70.5	4.4	332	3	US-08-875-533-2	Sequence 2, Appli	Sequence 2, Appli	368	70.5	4.4	1382	4	US-09-457-040B-7	Sequence 7, Appli
296	70.5	4.4	332	3	US-08-875-533-3	Sequence 3, Appli	Sequence 3, Appli	369	70.5	4.4	1698	3	US-09-315-793-12	Sequence 12, Appl
297	70.5	4.4	332	3	US-08-875-533-4	Sequence 4, Appli	Sequence 4, Appli	370	70	4.3	228	3	US-09-338-907-70	Sequence 70, Appl
298	70.5	4.4	332	3	US-08-875-533-5	Sequence 5, Appli	Sequence 5, Appli	371	70	4.3	228	4	US-09-218-207-70	Sequence 70, Appl
299	70.5	4.4	332	3	US-08-875-533-6	Sequence 6, Appli	Sequence 6, Appli	372	70	4.3	231	4	US-09-489-039A-8999	Sequence 8999, Ap
300	70.5	4.4	332	3	US-08-875-533-7	Sequence 7, Appli	Sequence 7, Appli	373	70	4.3	266	4	US-09-543-681A-4642	Sequence 4642, Ap
301	70.5	4.4	332	3	US-08-875-533-8	Sequence 8, Appli	Sequence 8, Appli	374	70	4.3	322	4	US-09-543-681A-6946	Sequence 6946, Ap
302	70.5	4.4	332	3	US-08-875-533-9	Sequence 9, Appli	Sequence 9, Appli	375	70	4.3	344	4	US-09-345-236B-67	Sequence 67, Appl
303	70.5	4.4	332	3	US-08-875-533-10	Sequence 10, Appl	Sequence 10, Appl	376	70	4.3	353	2	US-08-996-306-4	Sequence 4, Appli
304	70.5	4.4	332	3	US-08-875-533-11	Sequence 11, Appl	Sequence 11, Appl	377	70	4.3	353	3	US-09-338-907-4	Sequence 4, Appli
305	70.5	4.4	332	3	US-08-875-533-22	Sequence 22, Appl	Sequence 22, Appl	378	70	4.3	353	4	US-09-218-207-4	Sequence 4, Appli
306	70.5	4.4	332	3	US-08-875-533-66	Sequence 66, Appl	Sequence 66, Appl	379	70	4.3	364	2	US-08-996-306-5	Sequence 5, Appli
307	70.5	4.4	332	4	US-09-462-941-7	Sequence 7, Appli	Sequence 7, Appli	380	70	4.3	364	3	US-09-338-907-5	Sequence 5, Appli
308	70.5	4.4	332	5	PCT-US95-03776-25	Sequence 25, Appl	Sequence 25, Appl	381	70	4.3	364	4	US-09-218-207-5	Sequence 5, Appli
309	70.5	4.4	353	1	US-08-330-517-2	Sequence 2, Appli	Sequence 2, Appli	382	70	4.3	409	4	US-09-252-991A-29674	Sequence 29674, A
310	70.5	4.4	353	1	US-08-347-029-4	Sequence 4, Appli	Sequence 4, Appli	383	70	4.3	430	4	US-09-134-001C-4302	Sequence 4302, Ap
311	70.5	4.4	353	1	US-08-388-779A-2	Sequence 2, Appli	Sequence 2, Appli	384	70	4.3	442	3	US-09-252-292C-29	Sequence 29, Appl
312	70.5	4.4	353	1	US-08-484-246-1	Sequence 1, Appli	Sequence 1, Appli	385	70	4.3	451	4	US-09-086-663A-83	Sequence 83, Appl
313	70.5	4.4	353	1	US-08-591-070A-2	Sequence 2, Appli	Sequence 2, Appli	386	70	4.3	561	4	US-09-198-452A-744	Sequence 744, App
314	70.5	4.4	353	1	US-08-413-803-25	Sequence 25, Appl	Sequence 25, Appl	387	70	4.3	604	4	US-09-640-419C-23	Sequence 23, Appl
315	70.5	4.4	353	1	US-08-321-488A-25	Sequence 25, Appl	Sequence 25, Appl	388	70	4.3	620	3	US-09-000-145-1	Sequence 1, Appli
316	70.5	4.4	353	2	US-08-414-161B-2	Sequence 2, Appli	Sequence 2, Appli	389	70	4.3	641	4	US-09-543-681A-6258	Sequence 6258, Ap
317	70.5	4.4	353	2	US-08-457-254-4	Sequence 4, Appli	Sequence 4, Appli	390	70	4.3	761	4	US-09-328-352-7492	Sequence 7492, Ap
318	70.5	4.4	353	2	US-08-457-254-6	Sequence 6, Appli	Sequence 6, Appli	391	70	4.3	863	2	US-08-380-182-19	Sequence 19, Appl
319	70.5	4.4	353	2	US-08-927-855-2	Sequence 2, Appli	Sequence 2, Appli	392	70	4.3	863	2	US-08-380-182-20	Sequence 20, Appl



393	69.5	4.3	185	3	US-09-338-907-136	Sequence 136, App
394	69.5	4.3	185	4	US-09-218-207-136	Sequence 136, App
395	69.5	4.3	292	4	US-09-489-039A-12623	Sequence 12623, A
396	69.5	4.3	300	3	US-09-338-907-135	Sequence 135, App
397	69.5	4.3	300	4	US-09-218-207-135	Sequence 135, App
398	69.5	4.3	315	3	US-09-338-907-134	Sequence 134, App
399	69.5	4.3	315	4	US-09-218-207-134	Sequence 134, App
400	69.5	4.3	339	4	US-09-328-352-7424	Sequence 7424, Ap
401	69.5	4.3	393	4	US-09-489-039A-7305	Sequence 7305, Ap
402	69.5	4.3	436	3	US-08-669-378-6	Sequence 6, Appli
403	69.5	4.3	436	3	US-08-669-378-10	Sequence 10, Appl
404	69.5	4.3	468	4	US-09-252-991A-22538	Sequence 22538, A
405	69.5	4.3	474	4	US-09-252-991A-19624	Sequence 19624, A
406	69.5	4.3	488	4	US-09-489-039A-10133	Sequence 10133, A
407	69.5	4.3	534	4	US-09-252-991A-30678	Sequence 30678, A
408	69.5	4.3	566	4	US-09-252-991A-17799	Sequence 17799, A
409	69.5	4.3	604	4	US-09-134-000C-3870	Sequence 3870, Ap
410	69.5	4.3	807	4	US-09-252-991A-32992	Sequence 32992, A
411	69.5	4.3	925	4	US-09-924-097A-14	Sequence 14, Appli
412	69.5	4.3	1007	2	US-08-551-459-4	Sequence 4, Appli
413	69.5	4.3	1732	2	US-08-570-311-10	Sequence 10, Appl
414	69.5	4.3	1732	2	US-08-353-485-10	Sequence 10, Appl
415	69.5	4.3	2736	4	US-09-252-991A-30227	Sequence 30227, A
416	69	4.3	256	4	US-09-355-166-12	Sequence 12, Appl
417	69	4.3	302	4	US-09-252-991A-19817	Sequence 19817, A
418	69	4.3	344	4	US-09-489-039A-8542	Sequence 8542, Ap
419	69	4.3	378	2	US-08-846-762-87	Sequence 87, Appl
420	69	4.3	432	4	US-09-328-352-6798	Sequence 6798, Ap
421	69	4.3	448	4	US-09-198-452A-326	Sequence 326, App
422	69	4.3	452	4	US-09-215-418-2	Sequence 2, Appli
423	69	4.3	453	4	US-09-800-729-83	Sequence 83, Appl
424	69	4.3	456	4	US-09-328-352-6946	Sequence 6946, Ap
425	69	4.3	502	4	US-09-252-991A-23390	Sequence 23390, A
426	69	4.3	512	4	US-09-328-352-6192	Sequence 6192, Ap
427	69	4.3	600	3	US-08-904-871-3	Sequence 3, Appli
428	69	4.3	634	1	US-07-779-049-3	Sequence 3, Appli
429	69	4.3	634	1	US-08-080-240-3	Sequence 3, Appli
430	69	4.3	638	2	US-08-426-125-5	Sequence 5, Appli
431	69	4.3	638	2	US-08-455-355-5	Sequence 5, Appli
432	69	4.3	638	4	US-09-367-512-4	Sequence 4, Appli
433	69	4.3	661	4	US-09-107-532A-3677	Sequence 3677, Ap
434	69	4.3	749	4	US-09-252-991A-17331	Sequence 17331, A
435	69	4.3	836	4	US-09-254-352B-20	Sequence 20, Appl
436	69	4.3	983	3	US-09-252-991A-21667	Sequence 21667, A
437	69	4.3	1180	3	US-09-224-024-28	Sequence 28, Appl
438	69	4.3	1180	5	PCT-US94-07902-28	Sequence 28, Appl
439	69	4.3	1242	4	US-09-252-991A-25843	Sequence 25843, A
440	68.5	4.2	145	4	US-09-252-991A-28281	Sequence 28281, A
441	68.5	4.2	209	4	US-09-328-352-6086	Sequence 6086, Ap
442	68.5	4.2	297	4	US-09-489-039A-10089	Sequence 10089, A
443	68.5	4.2	322	4	US-09-199-637A-49	Sequence 49, Appl
444	68.5	4.2	350	4	US-09-489-039A-10384	Sequence 10384, A
445	68.5	4.2	379	4	US-09-417-197-129	Sequence 129, App
446	68.5	4.2	390	4	US-09-107-532A-4359	Sequence 4359, Ap
447	68.5	4.2	394	3	US-08-926-842B-60	Sequence 60, Appl
448	68.5	4.2	436	3	US-08-669-378-8	Sequence 8, Appli
449	68.5	4.2	502	1	US-08-484-840-3	Sequence 3, Appli
450	68.5	4.2	502	1	US-08-483-094-3	Sequence 3, Appli
451	68.5	4.2	505	1	US-08-123-161A-14	Sequence 14, Appl
452	68.5	4.2	505	1	US-08-483-278-14	Sequence 14, Appl
453	68.5	4.2	560	1	US-07-683-957B-1	Sequence 1, Appli
454	68.5	4.2	560	4	US-09-107-532A-4070	Sequence 4070, Ap
455	68.5	4.2	567	4	US-09-252-991A-27014	Sequence 27014, A
456	68.5	4.2	575	4	US-09-252-991A-16697	Sequence 16697, A
457	68.5	4.2	624	4	US-09-107-532A-6860	Sequence 6860, Ap
458	68.5	4.2	631	4	US-09-620-412C-325	Sequence 325, App
459	68.5	4.2	631	4	US-09-598-419-325	Sequence 325, App
460	68.5	4.2	772	2	US-08-714-677-2	Sequence 2, Appli
461	68.5	4.2	772	2	US-08-393-540-2	Sequence 2, Appli
462	68.5	4.2	772	2	US-08-714-537-2	Sequence 2, Appli
463	68.5	4.2	927	4	US-09-328-352-7922	Sequence 7922, Ap
464	68.5	4.2	1226	4	US-09-601-537-7	Sequence 7, Appli
465	68.5	4.2	1227	2	US-08-760-075A-18	Sequence 18, Appl
466	68.5	4.2	1227	3	US-09-338-546-18	Sequence 18, Appl
467	68.5	4.2	1227	4	US-09-659-084-18	Sequence 18, Appl
468	68.5	4.2	1297	4	US-09-107-532A-4552	Sequence 4552, Ap
469	68.5	4.2	1438	4	US-09-209-916-1	Sequence 1, Appli
470	68.5	4.2	1471	1	US-08-683-839B-3	Sequence 3, Appli
471	68.5	4.2	1661	2	US-08-882-083-2	Sequence 2, Appli
472	68.5	4.2	1661	3	US-08-558-107-2	Sequence 2, Appli
473	68.5	4.2	1661	3	US-09-243-539-2	Sequence 2, Appli
474	68.5	4.2	2332	1	US-07-864-004B-4	Sequence 4, Appli
475	68.5	4.2	2332	1	US-08-251-937A-4	Sequence 4, Appli
476	68.5	4.2	2332	1	US-08-212-133A-2	Sequence 2, Appli
477	68.5	4.2	2332	1	US-08-276-594A-2	Sequence 2, Appli
478	68.5	4.2	2332	1	US-08-474-503-2	Sequence 2, Appli
479	68.5	4.2	2332	2	US-08-670-707A-2	Sequence 2, Appli
480	68.5	4.2	2332	3	US-09-037-601-2	Sequence 2, Appli
481	68.5	4.2	2332	4	US-09-315-179-2	Sequence 2, Appli
482	68.5	4.2	2332	4	US-09-523-656-2	Sequence 2, Appli
483	68.5	4.2	2332	5	PCT-US93-03275-4	Sequence 4, Appli
484	68.5	4.2	2332	5	PCT-US94-13200-2	Sequence 2, Appli
485	68.5	4.2	2351	1	US-08-121-202-2	Sequence 2, Appli
486	68.5	4.2	2351	1	US-08-366-851A-2	Sequence 2, Appli
487	68.5	4.2	2351	4	US-10-133-907-4	Sequence 4, Appli
488	68.5	4.2	2351	6	5171844-2	Patent No. 5171844
489	68.5	4.2	2351	6	5422260-1	Patent No. 5422260
490	68.5	4.2	2409	6	5180808-2	Patent No. 5180808
491	68.5	4.2	2509	1	US-08-469-005A-10	Sequence 10, Appl
492	68	4.2	75	4	US-09-489-039A-10269	Sequence 10269, A
493	68	4.2	165	4	US-09-107-532A-6255	Sequence 6255, Ap
494	68	4.2	241	5	PCT-US91-08177-7	Sequence 7, Appli
495	68	4.2	265	4	US-09-198-452A-945	Sequence 945, App
496	68	4.2	281	4	US-09-252-991A-25471	Sequence 25471, A
497	68	4.2	436	4	US-09-734-673-2	Sequence 2, Appli
498	68	4.2	436	4	US-09-523-849-2	Sequence 2, Appli
499	68	4.2	437	4	US-09-134-001C-5342	Sequence 5342, Ap
500	68	4.2	481	4	US-09-894-998A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-09-621-976-4112  
; Sequence 4112, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4112  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -16...-1  
; NAME/KEY: UNSURE  
; LOCATION: 156  
; OTHER INFORMATION: Xaa = Lys,Arg  
US-09-621-976-4112

Query Match 13.6%; Score 220.5; DB 4; Length 185;  
Best Local Similarity 35.3%; Pred. No. 2.4e-17;  
Matches 60; Conservative 26; Mismatches 53; Indels 31; Gaps 6;  
QY 19 GIAVFLRGFFPAPVRSSARAEHGA--EPPAPEPSAGASNWTTLPPP-----LFSKVW 69  
Db 20 GIALFTSGFLLTRLELT---NHSSCQEPGPGP-----GSLPWGSGQKPGACWMASTRFVRV 71



US-09-540-236-2033  
Query Match 9.2%; Score 148; DB 4; Length 275;  
Best Local Similarity 23.0%; Pred. No. 1.4e-08;  
Matches 58; Conservative 45; Mismatches 119; Indels 30; Gaps 8;  
  
QY 66 SKVIVLIDALRDDVFVGSKGVKFMPTTYYLVEKGASHSFVAEAKPPTVTMPRIKALMTG 125  
Db 9 NKVILVVLDGLNADV----GLTCMGFLQALCEQHKAAYKLQCCLPSLRPLYECILTG 63  
QY 126 SLPGFVDVIRNLNSPALLEDVS---IROKAAGKRIVFYGDETWVK-----LFPKHFVE 176  
Db 64 VRPTDSGIYTHNQINRLSKEKSVMFYNCIQSNKVTAATAAYTWISELYNRSPFOAAFDRHTND 123  
QY 177 YDGTTSF--FVSDYTEVDNNV---TRHLDKVLKRGWDILILHYLGDLHIGHISGNPSPL 231  
Db 124 SSLPIQFGHFYDDAYEDSHLFDDADHLRKIYRP---DFLLVHSMNIDDAGHRFGLNSMQ 180  
QY 232 IGQLSEMSDVLMK-IHTSLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEENVNTPLI 290  
Db 181 YRNAARRADMILLSNYINLWLDDGYQ-----IIVTSDHGMMNDLSHGGNLIEREVPFY 233  
QY 291 LISSAFERKPGD 302  
Db 234 TIGDRFTNKQMD 245  
  
RESULT 4  
US-09-014-969-19  
; Sequence 19, Application US/09014969  
; Patent No. 5965397  
CENTRAL INTELLIGENCE AGENCY

APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John M.  
APPLICANT: LaVallie, Edward R.  
APPLICANT: Racie, Lisa A.  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Spaulding, Vikki  
APPLICANT: Agostino, Michael J.  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
TITLE OF INVENTION: ENCODING THEM  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,969

```

; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-09-014-969-19

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Query Match 8.6%; Score 139; DB 2; Length 355;  
Best Local Similarity 23.6%; Pred. No. 2.4e-07;  
Matches 63; Conservative 44; Mismatches 80; Indels 80; Gaps 12;  
QY 51 AGASSNWTLPPLFSKVVIVLIDALRDDDFVFGSKGVKFMPTTYLYLVEKG-----ASHSF 105  
Db 13 AALSLSLTFSLQPDQKQVLLVSDFGRWDYLYKVP-----TPHFHYIMKYGVHVQVNTNVF 68  
QY 106 VAEAKPPTVMPRIKALMTGSLP---GFV-----DVIRNLNSPALLEDSDVIRQAKAAGKR 157  
Db 69 I-----TKTYPNHYTLVTGLFAENHGIVANDMFDPIRKNKFS--LDHNMNIDSK----- 115  
QY 158 IVFYGDET--WV-----KLFPHKHFVEYDGTTSFFVSDYTEVDN 193  
Db 116 --FWEATPIWITNORAGHTSGAAMWPGTDVKIHKRFPHTYMPYNESVSF----- 163  
QY 194 NVTRHLDKVLKRGDW-----DILILHYLGLDHIGHISGPNPLIGQKLSMDSVLMKI 246  
Db 164 -----EDRVAKIVWFSTKEPINLGLLYWEDPDDMGHGLGPDSPLMGPPVISDIDKXLYL 218  
QY 247 HTSLOSKEKETPLPNLLVLCGDHGMSE 273  
Db 219 IQMLKKAKLWNTLN--LIITSDHGMTQ 243

RESULT 5  
US-09-187-331-2  
; Sequence 2, Application US/09187331  
; Patent No. 6043056  
; GENERAL INFORMATION:  
; APPLICANT: Yue, Henry  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Gorgone, Gina A.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS  
; FILE REFERENCE: PF-0631 US  
; CURRENT APPLICATION NUMBER: US/09/187,331  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PERL Program  
; SEQ ID NO 2  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: 2705267  
US-09-187-331-2

Query Match 7.9%; Score 127; DB 3; Length 438;  
Best Local Similarity 22.6%; Pred. No. 8.5e-06;  
Matches 53; Conservative 48; Mismatches 92; Indels 42; Gaps 10;  
QY 67 KVVIVLIDALRDDDFVFGSKGVKFMPTTYLYLVEKGASHSFVAEAKP--PTVTMPRIKALMT 124  
Db 25 KLLVFLLDGFRSDYI-SDEALESPLGFKFVSRGVKVDYLT---PDFPSLSYPNYVYTLMT 80  
QY 125 GSLPGFVDVIRN-----LNSPALL-----EDSVIRQAKAAGKRIVFYGD 163  
Db 81 GRHCEVHQMIGNYMWDPPTNKSFDIGVKNKDSMLPLWNGSEPLVWTLTKAKRKVYMYWYP 140  
QY 164 ETWVKLF---PKHFVEYDGTTSFFVSDYTEVD--NNVTRHLDKVLKRGDWDILILHYLGL 218  
Db 141 GCEVEILGVRPTYCLEYKNVP-----TDINFANAVSDALDS-FKSGRADLAAIYHERI 192  
QY 219 DHIGHISGPNPLIGQKLSMDSVLMKIHTSLOSKEKETPLPNLLVLCGDHGMSE 273  
Db 193 DVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLN--VIIFSDHGMTD 245

RESULT 6  
US-09-470-946-2

; Sequence 2, Application US/09470946  
; Patent No. 6358923  
; GENERAL INFORMATION:  
; APPLICANT: Yue, Henry  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Gorgone, Gina A.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS  
; FILE REFERENCE: PF-0631 US  
; CURRENT APPLICATION NUMBER: US/09/470,946  
; CURRENT FILING DATE: 1999-12-22  
; EARLIER APPLICATION NUMBER: US 09/187,331  
; EARLIER FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PERL Program  
; SEQ ID NO 2  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: 2705267  
US-09-470-946-2

Query Match 7.9%; Score 127; DB 4; Length 438;  
Best Local Similarity 22.6%; Pred. No. 8.5e-06;  
Matches 53; Conservative 48; Mismatches 92; Indels 42; Gaps 10;  
QY 67 KVVIVLIDALRDDDFVFGSKGVKFMPTTYLYLVEKGASHSFVAEAKP--PTVTMPRIKALMT 124  
Db 25 KLLVFLLDGFRSDYI-SDEALESPLGFKFVSRGVKVDYLT---PDFPSLSYPNYVYTLMT 80  
QY 125 GSLPGFVDVIRN-----LNSPALL-----EDSVIRQAKAAGKRIVFYGD 163  
Db 81 GRHCEVHQMIGNYMWDPPTNKSFDIGVKNKDSMLPLWNGSEPLVWTLTKAKRKVYMYWYP 140  
QY 164 ETWVKLF---PKHFVEYDGTTSFFVSDYTEVD--NNVTRHLDKVLKRGDWDILILHYLGL 218  
Db 141 GCEVEILGVRPTYCLEYKNVP-----TDINFANAVSDALDS-FKSGRADLAAIYHERI 192  
QY 219 DHIGHISGPNPLIGQKLSMDSVLMKIHTSLOSKEKETPLPNLLVLCGDHGMSE 273  
Db 193 DVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLN--VIIFSDHGMTD 245

RESULT 7  
US-09-187-331-6  
; Sequence 6, Application US/09187331  
; Patent No. 6043056  
; GENERAL INFORMATION:  
; APPLICANT: Yue, Henry  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Gorgone, Gina A.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS  
; FILE REFERENCE: PF-0631 US  
; CURRENT APPLICATION NUMBER: US/09/187,331  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PERL Program  
; SEQ ID NO 6  
; LENGTH: 873  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: g189650  
US-09-187-331-6

Query Match 6.2%; Score 101; DB 3; Length 873;  
Best Local Similarity 19.7%; Pred. No. 0.029;  
Matches 60; Conservative 45; Mismatches 115; Indels 84; Gaps 12;

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 2, 2004, 16:26:33 ; Search time 16 Seconds  
(without alignments)  
1863.711 Million cell updates/sec

Title: US-10-036-150-45  
Perfect score: 1617  
Sequence: 1 MRLSGTGFATCCVAIEVLGI.....LISSAFERKPGDIRHPRKHVQ 310

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : PIR 78:  
1: Pirl:  
2: Pirl:  
3: Pirl:  
4: Pirl:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	634.5	39.2	758	2	S62432	major facilitator
2	590	36.5	897	2	G84613	hypothetical prote
3	524	32.4	795	2	T21487	hypothetical prote
4	508.5	31.4	830	2	S50810	probable membrane
5	490.5	30.3	880	2	T02245	hypothetical prote
6	414	25.6	918	2	T40030	hypothetical prote
7	387	23.9	1017	2	S64782	probable membrane
8	347.5	21.5	905	2	A87794	protein C27A12.9 [
9	172.5	10.7	935	2	T40715	hypothetical prote
10	170	10.5	919	2	S37786	hypothetical prote
11	163.5	10.1	269	2	D81344	hypothetical prote
12	157	9.7	269	2	E83240	hypothetical prote
13	152.5	9.4	429	2	T33724	probable phosphodi
14	151	9.3	485	2	T40657	probable phosphodi
15	147	9.1	479	2	T03293	probable phosphodi
16	139	8.6	461	2	T09933	probable phosphodi
17	138	8.5	477	1	A59391	probable phosphodi
18	134	8.3	457	2	T09932	probable phosphodi
19	134	8.3	496	2	T09931	probable phosphodi
20	130	8.0	477	1	A59390	probable phosphodi
21	122.5	7.6	451	2	F87407	probable phosphodi
22	122	7.5	433	2	B82537	probable phosphodi
23	114	7.1	370	2	C71052	hypothetical prote
24	114	7.1	825	2	T46311	hypothetical prote
25	114	7.1	963	2	A57238	iron-responsive el
26	111.5	6.9	369	2	A75091	phosphonoacetate h
27	111.5	6.9	905	1	A27410	nucleotide diphosp
28	111	6.9	885	1	A55453	nucleotide diphosp
29	110.5	6.8	434	2	F96958	ap superfamily [im

30	108.5	6.7	520	2	D83845	hypothetical prote
31	101	6.2	743	2	S19437	hypothetical prote
32	101	6.2	925	1	A39216	nucleotide diphosp
33	96.5	6.0	2109	1	ZLVN	genome polyprotein
34	96	5.9	561	2	T05545	pollen-specific pr
35	95.5	5.9	513	2	A38193	phosphoprotein pho
36	94.5	5.8	388	2	F75162	tryptophan synthas
37	92	5.7	461	2	B90555	ABC transporter xy
38	92	5.7	521	2	C75320	glycyl-tRNA synthe
39	92	5.7	638	2	A33505	somatotropin recep
40	91.5	5.7	629	2	T22691	hypothetical prote
41	91.5	5.7	653	2	B81277	hypothetical prote
42	90.5	5.6	237	2	G89842	hypothetical prote
43	90.5	5.6	327	2	E35968	hypothetical expor
44	90.5	5.6	422	2	AB1252	pyrophosphatase ho
45	90.5	5.6	826	2	B36203	iron-responsive el
46	90.5	5.6	952	2	B57238	iron-responsive el
47	90	5.6	291	2	AD0949	hypothetical prote
48	90	5.6	634	2	S33339	somatotropin recep
49	89.5	5.5	291	2	AB1163	flagellar hook-ass
50	89.5	5.5	291	2	AB1522	flagellar hook-ass
51	89.5	5.5	300	1	H70557	probable acyl-CoA
52	89.5	5.5	510	2	S42705	probable phosphogl
53	89.5	5.5	604	2	H72712	probable RNase L i
54	89	5.5	359	1	A31425	uracil-DNA glycosy
55	89	5.5	700	2	A83434	conserved hypotet
56	89	5.5	891	2	T19915	hypothetical prote
57	88.5	5.5	258	1	OYECHF	imidazoleglycerol-
58	88.5	5.5	258	2	B90982	imidazoleglycerol-
59	88.5	5.5	258	2	H85827	imidazoleglycerol-
60	88.5	5.5	424	2	B95964	probable phosphono
61	88.5	5.5	802	2	C95136	conserved domain p
62	88.5	5.5	828	2	E98004	hypothetical prote
63	88	5.4	427	2	F83984	acetylornithine de
64	88	5.4	453	2	T16795	hypothetical prote
65	88	5.4	660	2	AD0661	invasin-like prote
66	87.5	5.4	1216	2	A28822	1-phosphatidylinos
67	87	5.4	314	2	A39374	Renilla-luciferin
68	87	5.4	875	1	A57080	cell surface antig
69	86.5	5.3	365	2	S36807	cytochrome P450 71
70	86.5	5.3	476	2	A46118	myosin-binding pro
71	86.5	5.3	519	2	I64163	hypothetical prote
72	86.5	5.3	527	2	E90740	probable enzyme [i
73	86.5	5.3	527	2	G85590	probable enzyme yb
74	86.5	5.3	527	2	G64818	probable membrane
75	86	5.3	485	2	I64157	hypothetical prote
76	86	5.3	496	2	T44987	aldehyde dehydroge
77	86	5.3	637	2	B83052	Dnak protein PA476
78	85.5	5.3	389	2	T43927	tryptophan synthas
79	85.5	5.3	390	2	T16746	hypothetical prote
80	85.5	5.3	913	2	T46339	hypothetical prote
81	85	5.3	378	2	B87304	N-acetylglucosamin
82	85	5.3	510	2	AH1381	phosphoglycerate m
83	85	5.3	510	2	AI1750	phosphoglycerate m
84	85	5.3	511	2	D97753	alkaline protease
85	85	5.3	677	2	S33608	somatotropin-bindi
86	85	5.3	906	2	G75362	aconitate hydratase
87	85	5.3	1098	2	S36868	alpha,alpha-trehal
88	85	5.3	1696	2	T00057	hypothetical prote
89	84.5	5.2	381	2	E72235	conserved hypotet
90	84.5	5.2	453	1	A59389	probable phosphodi
91	84.5	5.2	480	2	D75053	hypothetical prote
92	84.5	5.2	545	2	H83079	hypothetical prote
93	84.5	5.2	592	2	T15600	hypothetical prote
94	84.5	5.2	642	2	T41690	conserved hypotet
95	84.5	5.2	810	2	S75931	hypothetical prote
96	84	5.2	374	2	S75459	hypothetical prote
97	84	5.2	416	1	ITSH	alpha-1-antitrypsi
98	84	5.2	479	2	D30411	synapsin Iib - rat
99	84	5.2	585	2	C36858	G3R protein - vari
100	84	5.2	585	2	T28622	hypothetical prote
101	84	5.2	586	2	C30411	synapsin Iia - rat
102	83.5	5.2	336	1	S28412	carbonate dehydrat



103	83.5	5.2	349	2	T15082	hypothetical prote	176	79	4.9	637	2	JC5608	dnak-type molecula
104	83.5	5.2	482	2	C90067	hypothetical prote	177	79	4.9	638	2	S12136	somatotropin recep
105	83	5.1	331	1	S48675	carbonate dehydrat	178	79	4.9	907	2	T04820	aconitate hydrat
106	83	5.1	357	2	S73851	hypothetical prote	179	78.5	4.9	314	2	G69818	CMP-binding factor
107	83	5.1	400	2	B90001	hypothetical prote	180	78.5	4.9	501	2	B86351	protein disulfide-
108	83	5.1	472	2	AD1609	6-phosphogluconate	181	78.5	4.9	523	2	B71985	hypothetical prote
109	83	5.1	472	2	AD1246	6-phosphogluconate	182	78.5	4.9	545	2	S58970	carboxylesterase (
110	83	5.1	693	2	C83821	glycyl-tRNA synthe	183	78.5	4.9	549	2	S53427	protein-tyrosine-p
111	83	5.1	2175	1	S03170	homeotic protein c	184	78.5	4.9	600	2	A82043	inner membrane cop
112	83	5.1	3157	2	B70969	probable PPE prote	185	78.5	4.9	604	2	E75119	hypothetical prote
113	82.5	5.1	368	2	AF1185	alanine racemase h	186	78.5	4.9	608	2	AC0798	probable sodium/su
114	82.5	5.1	422	2	AD1614	weakly pyrophospha	187	78.5	4.9	609	2	S72845	H+-transporting tw
115	82.5	5.1	511	2	D71687	alkaline proteinas	188	78.5	4.9	656	1	A55574	protein-tyrosine-p
116	82.5	5.1	562	2	H70688	hypothetical prote	189	78.5	4.9	665	2	F97032	beta-glucosidase f
117	82.5	5.1	898	2	T10101	aconitate hydrat	190	78.5	4.9	674	2	F83794	ABC transporter (A
118	82.5	5.1	1398	2	T28159	cytoplasmic aconit	191	78.5	4.9	761	2	G70393	conserved hypothet
119	82.5	5.1	322	2	A82618	pyrolysin (EC 3.4.	192	78.5	4.9	775	2	S65769	maltooligosyl treh
120	82	5.1	972	2	T49773	hypothetical prote	193	78.5	4.9	804	2	A96494	protein F7F22.16 l
121	82	5.1	1458	2	S36014	related to actin-i	194	78.5	4.9	848	2	G86708	aconitate hydrat
122	82	5.1	1986	2	S28353	dynein heavy chain	195	78.5	4.9	1108	2	A55915	guanylate cyclase
123	82	5.0	352	2	A81136	probable polyketid	196	78.5	4.9	1173	1	A53430	1-phosphatidylinos
124	81.5	5.0	521	2	A33264	probable anthranil	197	78.5	4.9	1216	2	A28821	1-phosphatidylinos
125	81.5	5.0	521	2	A31257	phosphoprotein pho	198	78.5	4.9	1654	2	AI2067	two-component sens
126	81.5	5.0	525	2	F81017	phosphoprotein pho	199	78	4.8	242	2	AE1184	B. subtilis NagB p
127	81.5	5.0	548	2	E70807	probable fadD19 pr	200	78	4.8	290	2	AB2769	conserved hypothet
128	81.5	5.0	601	2	F83471	hypothetical prote	201	78	4.8	330	1	S61882	carbonate dehydrat
129	81.5	5.0	795	1	S73830	hypothetical prote	202	78	4.8	336	2	E84311	histidinol-phospha
130	81.5	5.0	940	2	B81852	endopeptidase La (	203	78	4.8	364	2	D97549	hypothetical prote
131	81.5	5.0	987	2	A75496	probable type III	204	78	4.8	432	2	T01925	hypothetical prote
132	81.5	5.0	1467	2	T48162	conserved hypothet	205	78	4.8	437	2	JC4929	transcription fact
133	81.5	5.0	490	2	G72352	hypothetical prote	206	78	4.8	465	2	H90508	cobryic acid synth
134	81	5.0	490	2	C70146	hypothetical prote	207	78	4.8	497	2	T15872	hypothetical prote
135	81	5.0	585	1	F64159	glutamate-tRNA lig	208	78	4.8	532	2	S54571	probable membrane
136	81	5.0	626	1	A48648	hypothetical prote	209	78	4.8	619	2	AI3336	potassium/proton a
137	81	5.0	1469	2	T19168	acetolactate synth	210	78	4.8	900	2	AI1279	aconitate hydrat
138	81	5.0	2078	2	T25400	hypothetical prote	211	78	4.8	1010	1	AJHUPR	phosphoribosylamin
139	81	5.0	258	1	OYEBHF	cyclase hisF - Sal	212	77.5	4.8	272	2	B95852	conserved hypothet
140	80.5	5.0	258	1	AI0764	cyclase hisF [limp	213	77.5	4.8	273	2	T34672	probable gntR fami
141	80.5	5.0	281	2	F97844	hypothetical prote	214	77.5	4.8	291	2	T37992	probable tricarbox
142	80.5	5.0	395	2	H75457	hypothetical prote	215	77.5	4.8	331	2	AC0842	glycine betaine-bi
143	80.5	5.0	491	2	AH3416	hypothetical prote	216	77.5	4.8	341	2	H90797	probable tellurium
144	80.5	5.0	505	2	C90569	AMP nucleosidase (	217	77.5	4.8	385	2	A85607	hypothetical prote
145	80.5	5.0	537	2	H64241	hypothetical prote	218	77.5	4.8	408	2	AH3269	dihydrolipoamide S
146	80.5	5.0	751	2	T30154	arginine-tRNA liga	219	77.5	4.8	451	2	H69006	DNA-directed RNA p
147	80.5	5.0	1036	2	S22383	hypothetical prote	220	77.5	4.8	478	2	JC4940	synapsin IIB - hum
148	80.5	5.0	1741	2	T13610	axonin 1 precursor	221	77.5	4.8	503	2	T20658	syntrophin-1 - mou
149	80.5	4.9	250	2	T08908	parallel sister ch	222	77.5	4.8	517	2	T20658	probable zinc meta
150	80	4.9	397	2	H72491	hypothetical prote	223	77.5	4.8	521	1	S35067	phosphoprotein pho
151	80	4.9	424	2	D89892	probable tyrosine	224	77.5	4.8	521	1	A56968	phosphoprotein pho
152	80	4.9	1813	2	T30564	dihydroorotate [im	225	77.5	4.8	540	2	T32230	hypothetical prote
153	79.5	4.9	270	2	G72390	resistance protei	226	77.5	4.8	545	2	S58980	carboxylesterase (
154	79.5	4.9	276	2	G75358	-dihydroorotate deh	227	77.5	4.8	545	2	S58979	carboxylesterase (
155	79.5	4.9	333	2	JC7139	hypothetical prote	228	77.5	4.8	545	2	S58974	carboxylesterase (
156	79.5	4.9	397	2	T35880	endo-1,4-beta-xyla	229	77.5	4.8	545	2	S58972	carboxylesterase (
157	79.5	4.9	416	2	A97093	hypothetical prote	230	77.5	4.8	545	2	S58975	carboxylesterase (
158	79.5	4.9	545	2	D90159	probable membrane	231	77.5	4.8	545	2	S58982	carboxylesterase (
159	79.5	4.9	560	1	F69059	hypothetical prote	232	77.5	4.8	545	2	S58983	carboxylesterase (
160	79.5	4.9	844	2	I37079	arginine-tRNA liga	233	77.5	4.8	545	2	S58976	carboxylesterase (
161	79.5	4.9	986	2	T03760	DNA ligase (ATP) (	234	77.5	4.8	545	2	S58968	carboxylesterase (
162	79.5	4.9	1072	2	A86827	pullulanase (EC 3.	235	77.5	4.8	545	2	S58981	carboxylesterase (
163	79.5	4.9	1090	2	A41696	hypothetical prote	236	77.5	4.8	567	2	E35928	hypothetical prote
164	79.5	4.9	1257	2	T01020	regulatory protein	237	77.5	4.8	579	2	F81711	conserved hypothet
165	79.5	4.9	2026	2	T02646	hypothetical prote	238	77.5	4.8	609	2	F70512	probable ATPase -
166	79.5	4.9	2535	2	AB0545	hypothetical prote	239	77.5	4.8	656	1	JC4263	protein-tyrosine-p
167	79	4.9	368	2	AE1543	probable transmemb	240	77.5	4.8	808	1	T04982	dynammin-like prote
168	79	4.9	372	2	T01600	alanine racemase h	241	77.5	4.8	875	2	F97850	DNA-directed DNA p
169	79	4.9	410	2	D70599	hypothetical prote	242	77.5	4.8	942	2	C96760	probable sucrose s
170	79	4.9	416	2	S21097	hypothetical prote	243	77.5	4.8	1021	2	T42634	connectin/titin -
171	79	4.9	427	2	A40735	alpha-1-antitrypsi	244	77.5	4.8	1423	2	A49206	exo-beta-D-fructos
172	79	4.9	511	2	T46865	TGF beta homolog d	245	77	4.8	175	2	B70730	probable lipoprote
173	79	4.9	610	2	A90459	phosphoglycerate m	246	77	4.8	211	2	H69403	conserved hypothet
174	79	4.9	632	2	G69306	hypothetical prote	247	77	4.8	280	2	AD2248	hypothetical prote
175	79	4.9				NADH oxidase (nox	248	77	4.8	372	2	T50014	trehalose-6-phosph

249	77	4.8	403	2	S58345	E2F-1 transcriptio	322	75.5	4.7	725	2	AB1187	conserved hypothet
250	77	4.8	564	2	T43298	transcription fact	323	75.5	4.7	820	2	T14879	hypothetical prote
251	77	4.8	631	2	A31203	interferon-regulat	324	75.5	4.7	878	2	T21621	hypothetical prote
252	77	4.8	878	1	A40091	interleukin-3 rece	325	75.5	4.7	900	2	D97351	sensor protein Kdp
253	77	4.8	1080	2	T03964	probable ubiquitin	326	75.5	4.7	932	2	G86857	isoleucine-tRNA li
254	77	4.8	1135	2	T30561	Scythe protein - A	327	75.5	4.7	968	2	C82452	hypothetical prote
255	77	4.8	1643	1	RRWGNV	genome polyprotein	328	75.5	4.7	982	2	S58881	mutS protein homol
256	77	4.8	2256	2	AD1018	large repetitive p	329	75.5	4.7	2504	1	A57788	enoyl-lacyl-carrie
257	76.5	4.7	295	2	F72777	hypothetical prote	330	75.5	4.7	3283	2	AC1018	large repetitive p
258	76.5	4.7	332	2	H86830	catabolite control	331	75	4.6	142	2	E84934	50S ribosomal prot
259	76.5	4.7	342	2	E82955	TonB protein PA553	332	75	4.6	244	2	A90786	probable synthetas
260	76.5	4.7	430	2	F81698	3-deoxy-manno-octu	333	75	4.6	244	2	G85645	probable synthetas
261	76.5	4.7	457	2	F71172	hypothetical prote	334	75	4.6	359	2	T01275	hypothetical prote
262	76.5	4.7	478	2	S06987	nitrogenase (EC 1.	335	75	4.6	364	2	S34355	peroxidase (EC 1.1
263	76.5	4.7	544	2	B40122	carboxylesterase (	336	75	4.6	407	2	B84993	phosphopentomutase
264	76.5	4.7	569	2	A97648	urease alpha chain	337	75	4.6	413	2	I56481	alpha 1-proteinase
265	76.5	4.7	569	2	AG2871	urease alpha subun	338	75	4.6	440	2	I61183	transcription fact
266	76.5	4.7	573	1	S33212	INDA1 protein - fu	339	75	4.6	453	2	H87373	hypothetical prote
267	76.5	4.7	585	2	D95419	Rhbc rhizobactin s	340	75	4.6	466	2	T11684	RVS167 protein hom
268	76.5	4.7	585	2	T46816	rhbc protein [limpo	341	75	4.6	469	2	A81836	probable 3-isoprop
269	76.5	4.7	710	1	C43497	early transcriptio	342	75	4.6	469	2	G81128	3-isopropylmalate
270	76.5	4.7	710	1	I42517	VERF, 82K subunit	343	75	4.6	485	2	AF3106	glutamyl-tRNA synt
271	76.5	4.7	710	2	T37394	conserved hypothet	344	75	4.6	488	2	F98180	glutamyl-tRNA synt
272	76.5	4.7	998	2	C75489	cardiomyosin-bi	345	75	4.6	501	2	C82414	aminopeptidase VCA
273	76.5	4.7	1064	2	C86795	hypothetical prote	346	75	4.6	536	2	G64752	xylan 1,4-beta-xy
274	76.5	4.7	1274	2	S55050	hypothetical prote	347	75	4.6	553	2	A89830	arginyl-tRNA synth
275	76.5	4.7	1295	2	T21720	hypothetical prote	348	75	4.6	711	2	T05291	arginine decarboxy
276	76.5	4.7	1383	2	T13052	guanine nucleotide	349	75	4.6	976	2	A36355	protein-tyrosine k
277	76	4.7	206	2	T36643	probable integral	350	75	4.6	1052	2	AG3206	AcrB/AcrD/AcrF fam
278	76	4.7	244	1	A64843	hypothetical prote	351	75	4.6	1086	2	JC6079	chitin synthase (E
279	76	4.7	322	2	H70462	quinolinate synthe	352	75	4.6	1244	2	T19068	hypothetical prote
280	76	4.7	345	2	E71254	hypothetical prote	353	75	4.6	1250	2	T40062	probable nuclear e
281	76	4.7	348	2	T02798	hypothetical prote	354	75	4.6	1338	2	T30565	MAP kinase kinase
282	76	4.7	376	2	T39454	hypothetical prote	355	75	4.6	1391	2	S73652	RNA polymerase bet
283	76	4.7	470	1	E64081	probable rhamnulok	356	75	4.6	3869	2	A48205	All-1 protein +GTE
284	76	4.7	493	2	S50443	probable phosphodi	357	74.5	4.6	233	2	B69900	conserved hypothet
285	76	4.7	511	2	D69675	phosphoglycerate m	358	74.5	4.6	255	2	A86894	30S ribosomal prot
286	76	4.7	514	2	T47556	pyruvate kinase-li	359	74.5	4.6	303	2	AH0082	LysR-family regula
287	76	4.7	616	2	JQ1441	hypothetical 67K p	361	74.5	4.6	366	1	W2WLR1	E2 protein - rhesu
288	76	4.7	638	2	B28176	somatotropin recep	362	74.5	4.6	464	2	E83029	replicative DNA he
289	76	4.7	659	2	F70453	aconitase - Aquife	363	74.5	4.6	467	2	T02238	glucosyl transfera
290	76	4.7	709	2	D82825	conserved hypothet	364	74.5	4.6	473	2	E75097	hypothetical prote
291	76	4.7	805	2	T37787	probable vacuolar	365	74.5	4.6	476	2	AI0080	ADP-heptose syntha
292	76	4.7	822	2	T01622	probable salt-indu	366	74.5	4.6	487	2	A69645	methylmalonate-sem
293	76	4.7	851	2	T38173	probable phosphati	367	74.5	4.6	504	2	S01074	L-arabinose transp
294	76	4.7	863	2	B71343	probable ribosomal	368	74.5	4.6	504	2	H09954	L-arabinose transp
295	76	4.7	907	2	AD2951	cell division prot	369	74.5	4.6	510	2	F96987	2,3-bisphosphoglyc
296	76	4.7	909	2	G69599	aconitase hydratase	370	74.5	4.6	513	2	S35132	2-isopropylmalate
297	76	4.7	910	2	H98331	cell division prot	371	74.5	4.6	521	2	T32231	hypothetical prote
298	76	4.7	944	2	T38130	probable helicase	372	74.5	4.6	532	2	B87496	protein-export mem
299	76	4.7	956	1	S53297	pyruvate, phosphat	373	74.5	4.6	532	2	I49329	retinoblastoma-ass
300	76	4.7	1068	2	A40265	retinoblastoma-ass	374	74.5	4.6	693	2	D97122	translation IF2, G
301	76	4.7	1165	1	GNLJGL	Hiv-1 retropepsin	375	74.5	4.6	709	1	AE3468	diguanylate cyclas
302	76	4.7	1512	2	T14883	hypothetical prote	376	74.5	4.6	710	1	H36848	early transcriptio
303	76	4.7	2137	2	T05244	hypothetical prote	377	74.5	4.6	710	2	E72164	A8L protein - vari
304	76	4.7	2366	2	S10317	toxin B - Clostrid	378	74.5	4.6	710	2	T28549	hypothetical prote
305	75.5	4.7	222	2	JQ0640	glutamine amidotra	379	74.5	4.6	715	2	S70397	zona pellucida gly
306	75.5	4.7	272	2	B75414	molybdenum cofacto	380	74.5	4.6	903	2	E88221	protein T01H3.2 [i
307	75.5	4.7	278	2	T18857	hypothetical prote	381	74.5	4.6	980	2	T24336	hypothetical prote
308	75.5	4.7	293	2	B89802	conserved hypothet	382	74.5	4.6	987	2	A64474	hypothetical prote
309	75.5	4.7	312	2	H64250	L-lactate dehydrog	383	74.5	4.6	992	2	T38817	hypothetical prote
310	75.5	4.7	332	2	AD2078	transcription regu	384	74.5	4.6	1036	2	AG1326	alpha-mannosidase
311	75.5	4.7	350	2	T33458	hypothetical prote	385	74.5	4.6	1061	2	I49328	retinoblastoma-ass
312	75.5	4.7	512	1	ISAASS	protein disulfide-	386	74.5	4.6	1104	2	A60999	alpha-amylase (EC
313	75.5	4.7	512	2	A41440	protein disulfide-	387	74.5	4.6	1178	2	S57698	regulatory protein
314	75.5	4.7	545	2	S58978	carboxylesterase (	388	74.5	4.6	1254	2	G86379	hypothetical prote
315	75.5	4.7	545	2	S58971	carboxylesterase (	389	74.5	4.6	1483	2	T19751	kinase-related pro
316	75.5	4.7	545	2	S58977	carboxylesterase (	390	74.5	4.6	2311	1	TVCHSR	genome polyprotein
317	75.5	4.7	545	2	S58973	carboxylesterase (	391	74.5	4.6	3432	1	GNWVUE	titin, cardiac mus
318	75.5	4.7	567	2	T30799	hypothetical prote	392	74.5	4.6	26926	1	I38344	chlorophyll a/b-bi
319	75.5	4.7	567	2	A42509	E6R protein - vacc	393	74	4.6	252	2	T51616	mab-18 protein (tr
320	75.5	4.7	568	1	A05225	gamma-glutamyltran	394	74	4.6	284	2	S60250	
321	75.5	4.7	669	2	T51220	hypothetical prote							

395	74	4.6	296	2	S60251	mab-18 protein (tr
396	74	4.6	329	1	S61884	carbonate dehydrat
397	74	4.6	350	2	AE3171	ATP-dependent DNA
398	74	4.6	361	2	D75039	hypothetical prote
399	74	4.6	380	2	H69427	probable 2,3-bisph
400	74	4.6	439	2	AE1251	probable peptidogl
401	74	4.6	474	2	T10271	capsid-associated
402	74	4.6	491	1	S60252	paired box transcr
403	74	4.6	502	1	JC1283	phosphoprotein pho
404	74	4.6	508	2	E96804	probable thioredox
405	74	4.6	538	2	T49418	hypothetical prote
406	74	4.6	618	2	E83853	hypothetical prote
407	74	4.6	621	2	JC5164	acetolactate synth
408	74	4.6	709	2	A86349	F8K7.2 protein - A
409	74	4.6	709	2	T16584	hypothetical prote
410	74	4.6	743	2	C56695	transducin-like en
411	74	4.6	838	2	T40203	conserved hypothet
412	74	4.6	960	2	A82187	probable cell divi
413	74	4.6	1038	2	AG2187	hypothetical prote
414	74	4.6	1143	4	I84547	hypothetical mdl f
415	74	4.6	1680	2	T41628	probable transcrip
416	74	4.6	2367	2	S70172	toxin B - Clostrid
417	74	4.6	4845	2	T31067	BIR repeat contain
418	73.5	4.5	146	1	HBNU21	hemoglobin beta-II
419	73.5	4.5	208	2	S09671	probable membrane
420	73.5	4.5	208	2	F90751	hypothetical prote
421	73.5	4.5	273	2	T03254	probable carbonate
422	73.5	4.5	298	2	T39491	4-nitrophenylphosp
423	73.5	4.5	318	2	T35984	probable riboflavi
424	73.5	4.5	359	2	D95876	conserved hypothet
425	73.5	4.5	397	2	AG0156	mannonate dehydrat
426	73.5	4.5	447	2	C96497	glyceraldehyde-3-p
427	73.5	4.5	462	2	AC2274	cytochrome P450 [1
428	73.5	4.5	505	2	H89850	hypothetical prote
429	73.5	4.5	507	2	AF0974	phosphoglycerate m
430	73.5	4.5	514	2	S47833	probable phosphogl
431	73.5	4.5	514	2	B91190	hypothetical prote
432	73.5	4.5	514	2	C86037	hypothetical prote
433	73.5	4.5	544	2	A34089	carboxylesterase (
434	73.5	4.5	544	2	C41426	carboxylesterase (
435	73.5	4.5	544	2	A41426	carboxylesterase (
436	73.5	4.5	548	2	A28022	carboxylesterase (
437	73.5	4.5	725	2	AI1544	conserved hypothet
438	73.5	4.5	764	2	E95252	conserved hypothet
439	73.5	4.5	764	2	C98117	conserved hypothet
440	73.5	4.5	805	2	T49385	hypothetical prote
441	73.5	4.5	1044	2	S01966	GTPase-activating
442	73.5	4.5	1065	2	A70797	hypothetical prote
443	73.5	4.5	1091	2	T13170	diaphanous protein
444	73.5	4.5	1149	2	T27567	hypothetical prote
445	73.5	4.5	1944	2	A55117	tsg24 protein - mo
446	73.5	4.5	2535	2	T04824	hypothetical prote
447	73	4.5	200	2	S72612	RNA helicase II -
448	73	4.5	266	2	B87498	hypothetical prote
449	73	4.5	276	2	E83889	chitoooligosacchari
450	73	4.5	332	2	B89791	hypothetical prote
451	73	4.5	336	2	AF2162	UDP-glucose 4-epim
452	73	4.5	343	2	E95911	probable transcrip
453	73	4.5	470	1	P2WL39	L2 protein - human
454	73	4.5	476	2	F87324	hypothetical prote
455	73	4.5	477	2	AC2834	UDP-MurNAC-pentape
456	73	4.5	477	2	G97611	UDP-N-acetylmuramo
457	73	4.5	533	2	AG2328	2,3-bisphosphoglyc
458	73	4.5	537	2	B81734	Aas bifunctional p
459	73	4.5	537	2	AG3572	oligopeptide-bind
460	73	4.5	564	2	T38291	GATA-type transcri
461	73	4.5	592	2	F95277	probable dihydroxy
462	73	4.5	618	2	F70855	probable ilvB prot
463	73	4.5	632	2	E69407	NADH oxidase (noxB
464	73	4.5	635	2	B82273	dnaK protein VC085
465	73	4.5	662	2	G86428	F26G16.2 protein -
466	73	4.5	708	2	A95214	cell wall surface
467	73	4.5	719	2	B98078	hypothetical prote
468	73	4.5	815	2	AG0057	hypothetical prote
469	73	4.5	824	2	F87330	photosynthesis pro
470	73	4.5	860	2	T15778	hypothetical prote
471	73	4.5	867	2	T41308	hypothetical zinc-
472	73	4.5	895	2	A84640	probable ligand-ga
473	73	4.5	912	2	S59861	band 3 anion trans
474	73	4.5	917	2	T04661	hypothetical prote
475	73	4.5	1036	2	AG3074	cation efflux syst
476	73	4.5	1036	2	B98212	cation efflux syst
477	73	4.5	1057	2	S47151	outer capsid prote
478	73	4.5	1076	2	A69409	carbamoyl-phosphat
479	73	4.5	1125	2	T09835	phytochrome A - Po
480	73	4.5	1225	2	T09395	envelope polyprote
481	73	4.5	1379	2	JC4954	vascular endotheli
482	73	4.5	4644	1	A38905	dynein heavy chain
483	72.5	4.5	223	1	Q0BE26	BZLF2 protein - hu
484	72.5	4.5	245	2	T48299	hypothetical prote
485	72.5	4.5	258	2	B54052	cyclase hisF - Kle
486	72.5	4.5	315	2	A57147	regulatory protein
487	72.5	4.5	344	2	D83894	hypothetical prote
488	72.5	4.5	359	2	D97651	hypothetical prote
489	72.5	4.5	368	2	E87753	protein C43E11.5 [
490	72.5	4.5	368	2	T29779	hypothetical prote
491	72.5	4.5	385	2	E70047	conserved hypothet
492	72.5	4.5	398	2	T41600	probable pre-mRNA
493	72.5	4.5	436	2	A75311	histidinol dehydro
494	72.5	4.5	505	2	AD2983	hypothetical prote
495	72.5	4.5	505	2	C98300	hypothetical prote
496	72.5	4.5	523	2	S67271	hypothetical prote
497	72.5	4.5	537	2	S73612	arginine-tRNA liga
498	72.5	4.5	542	2	AB0792	glycerol-3-phospha
499	72.5	4.5	550	2	AI2249	exopolysphatase
500	72.5	4.5	554	2	E83618	malonate decarboxy

ALIGNMENTS

RESULT 1

S62432  
 major facilitator protein homolog - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 16-May-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
 C:Accession: S62432; T37638  
 R:Odell, C.; Bowman, S.  
 submitted to the EMBL Data Library, October 1995  
 A:Reference number: S62430  
 A:Accession: S62432  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-758 <ODE>  
 A:Cross-references: EMBL:Z54308; NID:G1008985; PIDN:CAA91096.1; PID:G1008988  
 R:Odell, C.; Bowman, S.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.  
 submitted to the EMBL Data Library, October 1995  
 A:Reference number: Z21734  
 A:Accession: T37638  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-758 <OD2>  
 A:Cross-references: EMBL:Z54308; PIDN:CAA91096.1; GSPDB:GN00066; SPDB:SPAC13G6.03  
 A:Experimental source: strain 972h-; cosmid cl3G6  
 C:Genetics:  
 A:Gene: SPAC13G6.03  
 A:Map position: 1L

Query Match 39.2%; Score 634.5; DB 2; Length 758;

Best Local Similarity 46.2%; Pred. No. 1.8e-43;

Matches 133; Conservative 50; Mismatches 76; Indels 29; Gaps 7;

QY 15 IEVLGIAVFLRGFPAPVRSSARAHEGAPPAPEPSAGASSNWITLPPPLFSKVIVLID 74

Db 11 LQIFGSILFLGFFPHKNDSTGK-----AMSNQES-PPAVIDQVFMVD 54





A;Cross-references: EMBL:Z49337; MIPS:YJL062w

C;Genetics:

A;Gene: SGD:LAS21

A;Cross-references: SGD:S0003598

A;Map position: 10L

C;Keywords: transmembrane protein

Query Match 31.4%; Score 508.5; DB 2; Length 830;  
Best Local Similarity 38.8%; Pred. No. 3.5e-33;  
Matches 119; Conservative 53; Mismatches 110; Indels 25; Gaps 9;

QY 10 TCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPAPPEPSAGASSNWTTLPPPLFSKV 69

Db 7 TCLSCAQLLAILLFIFFAPPRKIVLT-----GISKQDPQDRDLQDRP-----FQKLV 55

QY 70 IVLIDALRDDVFVFGSKGVKEMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPG 129

Db 56 FVIIDALRSDFLFDSQISHFNHVLNTGEAWGYTSFANPPTVTLPRKSIITGSTPS 114

QY 130 FVDVIRN---LNSPALLE-DSVIRQAKAAGKRIVFYGDETWVKLFPKHFEVY-DGTTSF 183

Db 115 FIDLLNVAQDIDSDNLSEHDSWLQOFIQHNTIREMGDDTWLKLFPQWFFADPTHSF 174

QY 184 FVSDYTEVDNNVTRHLDKVL--KRGDWDILILHYLGLDHIHISGPNPLGQKLSMD 241

Db 175 FVSDFTQVDNNVTRNLPGKLFQEWACWDVAILHYLGLDHIHISGPNPLGQKLSMD 234

QY 242 VLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILIS---SAFER 298

Db 235 ILKSIYDEV--LEHEDDDTLICVLGDHGMNELGNHGSAGETSAGLFLSPKLAQFAR 292

QY 299 KPGDIRH 305

Db 293 PESQVNY 299

RESULT 5

T02245

hypothetical protein P1.11659\_3 - human

C;Species: Homo sapiens (man)

C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 05-Nov-1999

R;Lamerdin, J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhardt-Schultz, K.; G

; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Attix, C.; Andreise, T.; Trankhei

submitted to the EMBL Data Library, March 1998

A;Authors: Duarte, S.; Lucas, S.; Bruce, R.; Thomas, P.; Quan, G.; Kronmiller, B.; Arell

A;Description: Sequence analysis of a human P1 clone containing the XRCC9 DNA repair ge

A;Reference number: Z14637

A;Accession: T02245

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-880 <LAM>

A;Cross-references: EMBL:AC004472; NID:g2984582; PIDN:AAC07985.1; PID:g2984587

C;Genetics:

A;Map position: 9

A;Introns: 89/3; 152/1; 200/1; 241/2; 294/3; 354/3; 435/1; 733/1; 802/1; 871/1

Query Match 30.3%; Score 490.5; DB 2; Length 880;

Best Local Similarity 40.1%; Pred. No. 1.1e-31;

Matches 115; Conservative 45; Mismatches 92; Indels 35; Gaps 9;

QY 19 GIAVFLRGFFPAPVRSSARAEHGA--EPPAPEPSAGASSNWTTLPPP-----LFSKV 69

Db 20 GIALFTSGFLTRLELT---NHSSCQEPGP-----GSLPWGSKQKPGACWMSRFSRV 71

QY 70 IVLIDALRDDVFVFGSKGVKEMPTTY-LVEKGASHS--FVAEAKPPTVTMPRIKALMTGS 126

Db 72 LVLDALRFDEA-----QPQSHRIEIQPHARLYRSQVDPPTTTMQRKALTGS 123

QY 127 LPGFVDVIRNLNSPALLEDSDVIRQAKAAGKRIVFYGDETWVKLFPKHFEVYDGTTSFVS 186

Db 124 LPTFIDAGSNFASHAIVEDNLKQLTSAGRRVVFMDGDDTWKDLFPFGAFSKAFFFPFSFNR 183

QY 187 DYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPNPLGQKLSMDSVLMKI 246

Db 184 DLDTVDNGILEHLYPTMDSGEWDVLAHFLGVDHCGHKGPHPEMAKLSQMDQVIQGL 243

QY 247 HTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILIS 293

Db 244 ---VERLENDT---LLVAVAGDHGWTNGDHGGDSELEVSAAFLYS 283

RESULT 6

T40030

hypothetical protein SPBC27B12.06 - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C;Accession: T40030

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.

submitted to the EMBL Data Library, December 1997

A;Reference number: Z21900

A;Accession: T40030

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-918 <WOO>

A;Cross-references: EMBL:AL021766; PIDN:CAA16901.1; GSPDB:GN00067; SPDB:SPBC27B12.06

A;Experimental source: strain 972h; cosmid c27B12

C;Genetics:

A;Gene: SPDB:SPBC27B12.06

A;Map position: 2

Query Match 25.6%; Score 414; DB 2; Length 918;

Best Local Similarity 32.4%; Pred. No. 1.9e-25;

Matches 105; Conservative 60; Mismatches 121; Indels 38; Gaps 11;

QY 3 LGSCTFATCCVAIEVL-----GIAVFLRGFF--PAPVRSSARAEHGAEPAP-EP SAGA 53

Db 16 IGWXYIQACIFFAIIILISNFYGLKSFDTGFLLRRAVLNQTSLCEN---PPADVREWKNS 72

QY 54 SSNWTTLPPLPPLFSKVIVLIDALRDDDFVFGSKGVKFF-----MPYTYLVEKGASH--SF 105

Db 73 SGCWA--PKIFERAVIIVIDALRYDFLIPYNDNYYHNAFTTPTYETSVLHPENSYLTOF 129

QY 106 VAEAKPPTVTMPRIKALMTGSLPGFVDVIRNLNSPALLEDSDVIRQAKAAGKRIVFYGD 165

Db 130 IADA--PTTTSQRLKGLTGTSLPTFIDLGSNAGTNIDEDNLLQWKS LDKQIVLLGDDT 187

QY 166 WVKLFPKHFEV--YDGTTSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHI 223

Db 188 WDVLFHDYLNELTSLQPAFSENVPLHGVNDKVNQYVFDYIKDANFDVLIHAYLGV D HVGH 247

QY 224 ISGPNPLIGQKLSMDSVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTE 283

Db 248 RLGPDPHTMRDKLNQMDRCVKEMMDLLDSDS-----TLLIVMGDHGMNDKNGHGGDSFD 300

QY 284 EVNTPLILISS-----AFERKPGDI 303

Db 301 EINSVLWMYSKKPTFGYKQPGKV 324

RESULT 7

S64782

probable membrane protein YJL031c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein L0929

C;Species: Saccharomyces cerevisiae

C;Date: 01-Aug-1995 #sequence\_revision 24-May-1996 #text\_change 19-Apr-2002

C;Accession: S64782

R;Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.

submitted to the Protein Sequence Database, May 1996

A;Reference number: S64775

A;Accession: S64782

A;Molecule type: DNA

A;Residues: 1-1017 <DUE>

A;Cross-references: EMBL:Z73136; NID:g1360215; PID:g1360216; GSPDB:GN00012; MIPS:YJL031c

A;Experimental source: strain S288c

C;Genetics: